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Nucleic Acids, Proteins, and Antibodies

Statement under 37 C.F.R. § 1.77(b)(4)

[1] This application refers to a "Sequence Listing" listed below, which is provided as an electronic document on two identical compact discs (CD-R), labeled "Copy 1" and "Copy 2." These compact discs each contain the following files, which are hereby incorporated in their entirety herein:

Document	File Name	Size in bytes	Date of Creation
Sequence Listing	PTZ32_seqList.txt	3,411,250	01/15/2001
V Viewer Setup File	SetupDLL.exe	695,808	12/19/2000
V Viewer Help File Controller	v.cnt	7,984	01/05/2001
V Viewer Program File	v.exe	753,664	12/19/2000
V Viewer Help File	v.hlp	447,766	01/05/2001

[2] The Sequence Listing may be viewed on an IBM-PC machine running the MS-Windows operating system by using the V viewer software, licensed by HGS, Inc., included on the compact discs (see World Wide Web URL: <http://www.fileviewer.com>).

Field of the Invention

[3] The present invention relates to novel proteins. More specifically, isolated nucleic acid molecules are provided encoding novel polypeptides. Novel polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human polynucleotides and/or polypeptides, and antibodies. The invention further relates to diagnostic and therapeutic

methods useful for diagnosing, treating, preventing and/or prognosing disorders related to these novel polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compositions for inhibiting or enhancing the production and function of the polypeptides of the present invention.

Background of the Invention

[4] One of the most critical tasks a cell must perform is to respond to cues from its environment, i.e., extracellular signals. Some of the most important extracellular signals come from other cells. The ability for cells to be able to send and receive signals from one another is of paramount importance in multicellular organisms because it allows individual cells within a body to become highly specialized and yet work in a coordinated fashion with other cells of the body. Cellular signaling mechanisms regulate a variety of cellular processes such as, for example, proliferation, differentiation, survival, movement, and secretion. Defects in cellular signaling can lead to a number of diseases and disorders such as cancers, immune system disorders and nervous system disorders. For more expansive reviews on this subject, please refer to Hunter, *Cell* 100:113-127 and Chapter 15 of *Molecular Biology of the Cell*, Third Edition, edited by Alberts et al. (1994), which are herein incorporated by reference in their entirety.

[5] Signal transduction requires molecules that serve as the extracellular signaling molecules as well as a set of receptors that "receive" the signal. Frequently, an additional set of proteins is necessary in order for the cell to translate the signal it has received into an appropriate response via the activation or inhibition of a particular set of genes or proteins. The signaling molecules, the receptor proteins, and the molecules that relay the signal between the receptor and the final effector molecules collectively form what are known as signal transduction pathways.

[6] To date, several common types of signal transduction pathways have been identified. One way to classify a signal transduction pathway is based on the class of receptor protein it utilizes. Two well known classes of receptor proteins are G-protein coupled receptors and enzyme-linked receptors. This latter class of enzyme-linked receptors includes receptor tyrosine kinases, tyrosine kinase associated receptors, receptor serine/threonine kinases, receptor tyrosine phosphatases, and receptor guanylyl cyclases.

Signal Transduction through G-protein Coupled Receptors

[7] G protein coupled receptors are the largest family of cell surface receptors. They are seven-pass transmembrane receptors which activate trimeric G proteins (G proteins) upon ligand binding. G proteins are GTPases composed of three subunits: alpha, beta and gamma. G proteins function as molecular switches existing in two states: an active GTP bound state and an inactive GDP bound state. Ligand binding to G protein coupled receptors induce inactive G proteins to release GDP allowing GTP to bind in its place. Binding of GTP to a G protein causes the alpha subunit to dissociate from the beta and gamma subunits which remain associated with one another. Eventually, the GTPase activity of the alpha subunit results in hydrolysis of the bound GTP molecule to GDP, thus inactivating the G protein.

[8] There are several types of G proteins that have been classified based upon their function. Stimulatory G proteins (G_s) are involved in adenylate cyclase activation; inhibitory G proteins (G_i) function to inhibit the activity of adenylate cyclase. Yet another type of G protein, G_q proteins, functions in the activation of phosphoinositide-specific phospholipase C enzyme.

[9] Activation of adenylate cyclase by an activated G_s protein results in the production of the cyclic nucleotide, cyclic AMP (cAMP). cAMP mediates its effects mostly through its activation of cAMP dependent kinase (A-kinase), a serine/threonine kinase. Activation of A-kinase helps to further relay the signal from the G protein coupled receptor to the target proteins. In muscle cells, for instance, activation of A-kinase following adrenaline signaling ultimately results in the activation of an enzyme, glycogen phosphorylase, which catalyzes the release of glucose molecules which can be used to produce energy from glycogen. In other instances, activated A-kinase translocates to the nucleus where it phosphorylates the cAMP response element binding (CREB) protein, which when phosphorylated, acts as a transcription factor to stimulate the expression of genes that have cAMP response elements (CRE) sequences in their regulatory regions.

[10] G_q proteins, when activated, activate the enzyme phospholipase C-beta which hydrolyzes PI 4,5-bisphosphate (PIP_2) producing inositol triphosphate (IP_3) and diacylglycerol (DAG). IP_3 functions as a second messenger that causes the release of Ca^{2+} from intracellular stores. Released calcium then binds to Ca^{2+} binding proteins such as calmodulin, which in its calcium bound state, is able to activate Ca^{2+} /calmodulin dependent protein kinases (CaM-kinases). Activated CaM kinases then continue to relay the signal to

more downstream molecules in the signal transduction pathway. The other product produced by phospholipase C-beta, DAG, functions to activate the serine/threonine kinase known as protein kinase C (PKC). Activated PKC phosphorylates target proteins depending on the cell type, and in many cells these phosphorylation events lead to the increased transcription of specific genes. The highest concentrations of protein kinase C are found in the brain where PKC phosphorylates ion channels in nerve cells thereby altering their excitability. PKC activation can be induced by treating cells with phorbol esters which are able to cross the plasma membrane, bind to, and activate PKC directly.

Signal Transduction through Receptor Tyrosine Kinases

[11] The receptor protein tyrosine kinases (RPTKs) are some of the most well studied receptors, and the signaling cascades they initiate demonstrate two of the fundamental concepts in signal transduction: the regulation of protein phosphorylation and the recruitment of proteins into a signaling cascade via protein-protein interaction domains.

[12] Binding of the cognate ligand to a RPTK, such as epidermal growth factor (EGF) binding to the epidermal growth factor receptor (EGFR), induces RPTKs to dimerize and cross-phosphorylate each other on multiple tyrosine residues. The phosphorylated receptor dimer is the activated form of the receptor.

[13] The phosphorylated tyrosines on activated RPTKs are then recognized/bound by other components of the signal transduction pathway. One of the important discoveries in the field of signal transduction was the recognition of conserved domains which allow for protein-protein interactions in signaling pathways. The most prevalent binding domain that recognizes phosphotyrosine (P-Tyr) residues is known as the SH2 domain (for Src homology region 2, named after the Src protein in which the SH2 domain was first discovered). Another domain that recognizes P-Tyr residues is called the P-Tyr binding domain (PTB). The discovery of the SH2 domain was quickly followed by the discovery of several other protein-protein interaction domains involved in signal transduction and by the realization that most of these domains are modular in nature, meaning these domains fold independently – a most convenient feature for protein engineering. To date, more than 100 such protein interaction domains involved in signaling have been defined via comparative sequence analysis. Most of these domains recognize short linear sequences (approximately 4-10 amino acid residues in length), in some cases requiring phosphorylation of specific residues within the sequence allowing for inducible association. A convenient web based database, with

links to abstracts of papers characterizing these domains can be found at <http://smart.EMBL-Heidelberg.de>.

[14] Proteins containing SH2 and PTB domains translocate to the plasma membrane where they associate with the activated RPTKs which, in turn, activates them through phosphorylation. By way of example, activation of the platelet derived growth factor receptor (PDGFR) results in the autophosphorylation of tyrosine residues in the cytoplasmic tail of the PDGFR. These P-Tyr residues then serve as the binding sites for other proteins, such as a GTPase (discussed in more detail below), phospholipase C-gamma, and the regulatory subunit of PI-3-kinase, which are each able to recognize the P-Tyr residues in PDGFR via SH2 domains. The interaction of these proteins with the activated PDGFR results in the translocation of these proteins to the plasma membranes where they have their substrates and the PDGFR mediated activation of these proteins via phosphorylation.

[15] In the previous example, each of the proteins recruited to the activated RPTK via their SH2 domains also had catalytic activities that allowed them to propagate a signal. There are proteins involved in signal transduction, however, which have no ability in and of themselves to propagate a signal. Instead, these proteins, known as adaptor proteins, serve to couple activated RPTKs to other components of the signal transduction pathway which do have the capacity to propagate the signal. One such adaptor protein is known as Grb2. It contains one SH2 domain and two SH3 domains (another Src homology domain that mediates protein interactions). Grb 2 is constitutively associated with Sos protein, a guanine nucleotide releasing protein (GNRP), via its SH3 domain. Thus, when Grb2 associates with an activated receptor via its SH2 domain, it also brings Sos into proximity with the RPTK which activates the Sos protein via phosphorylation.

[16] GNRP proteins, such as Sos, are one of two types of proteins that help regulate the activity of proteins belonging to the Ras superfamily of monomeric GTPases. Ras proteins are proteins that are associated with the cytoplasmic side of the plasma membrane and help relay signals from RPTK to the nucleus to stimulate cell proliferation or differentiation. Ras proteins exist in two states, an inactive state in which ras is bound to GDP and an active state in which ras is bound to GTP. Activated GNRP proteins promote the exchange of bound GDP for GTP on ras proteins, thereby activating ras. Ras, itself, is a GTPase that hydrolyzes GTP to GDP, and would therefore tend to inactivate itself over time. However, ras is an inefficient GTPase, so the inactivation of ras is enhanced by GTPase activating proteins (GAPs) which increase the rate of hydrolysis of GTP by ras.

[17] Activated Ras kinases then act to activate more downstream signaling events, including activation of the mitogen-activated protein kinase (MAPK) pathway which is a cascade of serine/threonine kinases. Ras binds to and activates a MAPK kinase kinase (MAPKKK, such as Raf-1, for example), which in turn activates a MAPK kinase (MAPKK) via phosphorylation, which in turn activates a MAPK. MAPKs relay signals downstream by phosphorylating various proteins in the cell including other kinases and/or regulatory proteins in the cell. For instance, an activated MAPK can enter the nucleus and help to initiate transcription of genes that must be expressed in order for the cell to respond to the extracellular signal, such as genes required for DNA replication in response to the extracellular proliferation signal.

[18] Another class of signaling receptors, receptor serine/threonine kinases (RSK) has recently been identified. An example of an RSK is the TGF-beta receptor. Additionally, it has also been recently recognized that there are modular binding domains that recognize phosphoserine/phosphothreonine (P-Ser/P-Thr) residues. For instance, 14-3-3 domains recognize phosphoserines in specific amino acid contexts [RSX(P-Ser)XP] or [R(Y/F)X(P-Ser)XP] and may function in the assembly of signaling complexes. Other residues such as histidine and arginine can also be phosphorylated, and it is possible that additional kinases which phosphorylate these residues, or protein domains that bind phosphohistidine or phosphoarginine will be discovered.

Signaling Via Intracellular Receptors

[19] Some extracellular signals do not have cell surface receptors such as G protein coupled receptors or receptor tyrosine kinases. Instead, these extracellular signals are able to traverse the plasma membrane and interact with their receptors in the cytoplasm. Examples of such signals are the steroid hormones and the gas nitrous oxide (NO). The steroid hormone receptors, once bound by their ligand, are generally able to translocate to the nucleus where they bind regulatory DNA elements that control the gene expression of specific genes. NO gas, on the other hand, generally enters a cell and reacts with iron in the active site of the enzyme guanylate cyclase, stimulating it to produce cyclic GMP (cGMP). cGMP acts as a second messenger (similar to the way cAMP functions) and can stimulate further downstream signaling by binding to other proteins.

Terminating Signal Transduction

[20] As the effects of signal transduction are transient, there must also be mechanisms for terminating signal cascades. For example, G proteins are self-inactivating, and there are a set of proteins, GAPs, that are devoted to increasing the rate of hydrolysis of bound GTP by ras proteins. Cyclic nucleotide second messengers such as cAMP and cGMP are hydrolyzed by phosphodiesterases. In the case of kinases, there generally exist a set of complementary phosphatases that function to dephosphorylate phosphorylated residues, thereby bringing the signaling event to a close.

Signal Transduction Pathway Components and Disease

[21] Because signal transduction is involved in the regulation of so many cellular processes, including proliferation, differentiation, survival, and apoptosis, it is not surprising that defects in cellular signal transduction pathway components lead to a number of diseases and disorders, especially cancers. For a review on Signal transduction pathway components and diseases, see Hunter, Philosophical Transactions of the Royal Society of London Series B 353:583-605 (1998) which is herein incorporated by reference in its entirety. For instance, approximately 30% of human cancers have mutations in a ras gene, and at least 18 tyrosine kinases have been identified as oncogenes in either acutely transforming retroviruses or in human tumors, such as for example, Src. And more than 95% of chronic myelogenous leukemias express an activated form of the c-Abl non-receptor tyrosine kinases.

[22] Mutations in signaling pathways are also implicated in a plethora of other diseases. Mutation in Bruton's tyrosine kinase leads to X-linked agammaglobulinemia. Inactivation of ZAP70 or JAK3 leads to a severe combined immunodeficiency disease. Coffin-Lowry syndrome occurs when the X-linked Rsk2 protein serine kinase gene is inactivated. Myotonic dystrophy occurs when expression of the myotonic dystrophy serine kinase gene is decreased. Overexpression of the aurora2 serine kinase is implicated in colon carcinoma.

[23] The malfunction of signal transduction pathway components, particularly kinases, in diseases indicate that these genes are good targets for drugs/pharmaceuticals that either inhibit or activate their function. In fact, some such drugs have been developed and are already in use or in clinical trials. For instance, an inhibitor of cyclin dependent kinase 2 (cdk2), a kinase important in regulating cellular proliferation, is in clinical trials for cancer treatment, as are inhibitors of epidermal growth factor receptor tyrosine kinases and vascular endothelial growth factor receptor (VEGFR) tyrosine kinases. Inhibition of VEGFR activity

reduces or eliminates the vascularization of tumors directed by VEGFR. An antagonistic monoclonal antibody, herceptin, against the erbB2 receptor tyrosine kinase is being used in breast cancer therapies to treat breast cancers where ErbB2 is overexpressed.

[24] Thus there exists a clear need for identifying and exploiting novel signal transduction pathway component polynucleotides and polypeptides. Although structurally related, such proteins may possess diverse and multifaceted functions in a variety of cell and tissue types. The inventive purified signal transduction pathway component polypeptides are research tools useful for the identification, characterization and purification of additional proteins involved in signal transduction. Furthermore, the identification of new signal transduction pathway component polynucleotides and polypeptides permits the development of a range of derivatives, agonists and antagonists at the nucleic acid and protein levels which in turn have applications in the treatment and diagnosis of a range of conditions such as, for example, cancer and other proliferative disorders (e.g., chronic myelogenous leukemia), immunological disorders (e.g., severe combined immunodeficiency and X-linked agammaglobulinemia), and nervous system disorders (Coffin-Lowry Syndrome), amongst other conditions.

Summary of the Invention

[25] The present invention relates to novel proteins. More specifically, isolated nucleic acid molecules are provided encoding novel polypeptides. Novel polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human polynucleotides and/or polypeptides, and antibodies. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to these novel polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compositions for inhibiting or enhancing the production and function of the polypeptides of the present invention.

Detailed Description

Tables

[26] Table 1A summarizes some of the polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:)) and contig nucleotide sequence identifier (SEQ ID NO:X)) and further summarizes certain characteristics of these polynucleotides and the polypeptides encoded thereby. The first column provides the gene number in the application for each clone identifier. The second column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence disclosed in Table 1A. The third column provides a unique contig identifier, "Contig ID:" for each of the contig sequences disclosed in Table 1A. The fourth column provides the sequence identifier, "SEQ ID NO:X", for each of the contig sequences disclosed in Table 1A. The fifth column, "ORF (From-To)", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:X that delineate the preferred open reading frame (ORF) that encodes the amino acid sequence shown in the sequence listing and referenced in Table 1A as SEQ ID NO:Y (column 6). Column 7 lists residues comprising predicted epitopes contained in the polypeptides encoded by each of the preferred ORFs (SEQ ID NO:Y). Identification of potential immunogenic regions was performed according to the method of Jameson and Wolf (CABIOS, 4; 181-186 (1988)); specifically, the Genetics Computer Group (GCG) implementation of this algorithm, embodied in the program PEPTIDESTRUCTURE (Wisconsin Package v10.0, Genetics Computer Group (GCG), Madison, Wisc.). This method returns a measure of the probability that a given residue is found on the surface of the protein. Regions where the antigenic index score is greater than 0.9 over at least 6 amino acids are indicated in Table 1A as "Predicted Epitopes". In particular embodiments, polypeptides of the invention comprise, or alternatively consist of, one, two, three, four, five or more of the predicted epitopes described in Table 1A. It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly. Column 8, "Tissue Distribution" shows the expression profile of tissue, cells, and/or cell line libraries which express the polynucleotides of the invention. The first number in column 8 (preceding the colon), represents the tissue/cell source identifier code corresponding to the key provided in Table 4. Expression of these polynucleotides was not observed in the other tissues and/or cell libraries tested. For those identifier codes in which the first two letters are not "AR", the second number in column 8 (following the colon), represents the number of times a sequence corresponding to the reference polynucleotide sequence (e.g., SEQ ID NO:X) was identified in the tissue/cell source. Those tissue/cell

source identifier codes in which the first two letters are "AR" designate information generated using DNA array technology. Utilizing this technology, cDNAs were amplified by PCR and then transferred, in duplicate, onto the array. Gene expression was assayed through hybridization of first strand cDNA probes to the DNA array. cDNA probes were generated from total RNA extracted from a variety of different tissues and cell lines. Probe synthesis was performed in the presence of ³³P dCTP, using oligo(dT) to prime reverse transcription. After hybridization, high stringency washing conditions were employed to remove non-specific hybrids from the array. The remaining signal, emanating from each gene target, was measured using a Phosphorimager. Gene expression was reported as Phosphor Stimulating Luminescence (PSL) which reflects the level of phosphor signal generated from the probe hybridized to each of the gene targets represented on the array. A local background signal subtraction was performed before the total signal generated from each array was used to normalize gene expression between the different hybridizations. The value presented after "[array code]:" represents the mean of the duplicate values, following background subtraction and probe normalization. One of skill in the art could routinely use this information to identify normal and/or diseased tissue(s) which show a predominant expression pattern of the corresponding polynucleotide of the invention or to identify polynucleotides which show predominant and/or specific tissue and/or cell expression. Column 9 provides the chromosomal location of polynucleotides corresponding to SEQ ID NO:X. Chromosomal location was determined by finding exact matches to EST and cDNA sequences contained in the NCBI (National Center for Biotechnology Information) UniGene database. Given a presumptive chromosomal location, disease locus association was determined by comparison with the Morbid Map, derived from Online Mendelian Inheritance in Man (Online Mendelian Inheritance in Man, OMIM™. McKusick-Nathans Institute for Genetic Medicine, Johns Hopkins University (Baltimore, MD) and National Center for Biotechnology Information, National Library of Medicine (Bethesda, MD) 2000. World Wide Web URL: <http://www.ncbi.nlm.nih.gov/omim/>). If the putative chromosomal location of the Query overlaps with the chromosomal location of a Morbid Map entry, an OMIM identification number is disclosed in column 10 labeled "OMIM Disease Reference(s)". A key to the OMIM reference identification numbers is provided in Table 5.

[27] Table 1B summarizes additional polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) contig nucleotide sequence identifiers (SEQ ID NO:X)), and genomic

sequences (SEQ ID NO:B). The first column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence. The second column provides the sequence identifier, "SEQ ID NO:X", for each contig sequence. The third column provides a unique contig identifier, "Contig ID:" for each contig sequence. The fourth column, provides a BAC identifier "BAC ID NO:A" for the BAC clone referenced in the corresponding row of the table. The fifth column provides the nucleotide sequence identifier, "SEQ ID NO:B" for a fragment of the BAC clone identified in column four of the corresponding row of the table. The sixth column, "Exon From-To", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:B which delineate certain polynucleotides of the invention that are also exemplary members of polynucleotide sequences that encode polypeptides of the invention (e.g., polypeptides containing amino acid sequences encoded by the polynucleotide sequences delineated in column six, and fragments and variants thereof).

[28] Table 2 summarizes homology and features of some of the polypeptides of the invention. The first column provides a unique clone identifier, "Clone ID NO:Z", corresponding to a cDNA clone disclosed in Table 1A. The second column provides the unique contig identifier, "Contig ID:" corresponding to contigs in Table 1A and allowing for correlation with the information in Table 1A. The third column provides the sequence identifier, "SEQ ID NO:X", for the contig polynucleotide sequence. The fourth column provides the analysis method by which the homology/identity disclosed in the Table was determined. Comparisons were made between polypeptides encoded by the polynucleotides of the invention and either a non-redundant protein database (herein referred to as "NR"), or a database of protein families (herein referred to as "PFAM") as further described below. The fifth column provides a description of the PFAM/NR hit having a significant match to a polypeptide of the invention. Column six provides the accession number of the PFAM/NR hit disclosed in the fifth column. Column seven, "Score/Percent Identity", provides a quality score or the percent identity, of the hit disclosed in columns five and six. Columns 8 and 9, "NT From" and "NT To" respectively, delineate the polynucleotides in "SEQ ID NO:X" that encode a polypeptide having a significant match to the PFAM/NR database as disclosed in the fifth and sixth columns. In specific embodiments polypeptides of the invention comprise, or alternatively consist of, an amino acid sequence encoded by a polynucleotide in SEQ ID NO:X as delineated in columns 8 and 9, or fragments or variants thereof.

[29] Table 3 provides polynucleotide sequences that may be disclaimed according to

certain embodiments of the invention. The first column provides a unique clone identifier, "Clone ID", for a cDNA clone related to contig sequences disclosed in Table 1A. The second column provides the sequence identifier, "SEQ ID NO:X", for contig sequences disclosed in Table 1A. The third column provides the unique contig identifier, "Contig ID:", for contigs disclosed in Table 1A. The fourth column provides a unique integer 'a' where 'a' is any integer between 1 and the final nucleotide minus 15 of SEQ ID NO:X, and the fifth column provides a unique integer 'b' where 'b' is any integer between 15 and the final nucleotide of SEQ ID NO:X, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:X, and where b is greater than or equal to a + 14. For each of the polynucleotides shown as SEQ ID NO:X, the uniquely defined integers can be substituted into the general formula of a-b, and used to describe polynucleotides which may be preferably excluded from the invention. In certain embodiments, preferably excluded from the invention are at least one, two, three, four, five, ten, or more of the polynucleotide sequence(s) having the accession number(s) disclosed in the sixth column of this Table (including for example, published sequence in connection with a particular BAC clone). In further embodiments, preferably excluded from the invention are the specific polynucleotide sequence(s) contained in the clones corresponding to at least one, two, three, four, five, ten, or more of the available material having the accession numbers identified in the sixth column of this Table (including for example, the actual sequence contained in an identified BAC clone).

[30] Table 4 provides a key to the tissue/cell source identifier code disclosed in Table 1A, column 8. Column 1 provides the tissue/cell source identifier code disclosed in Table 1A, Column 8. Columns 2-5 provide a description of the tissue or cell source. Codes corresponding to diseased tissues are indicated in column 6 with the word "disease". The use of the word "disease" in column 6 is non-limiting. The tissue or cell source may be specific (e.g. a neoplasm), or may be disease-associated (e.g., a tissue sample from a normal portion of a diseased organ). Furthermore, tissues and/or cells lacking the "disease" designation may still be derived from sources directly or indirectly involved in a disease state or disorder, and therefore may have a further utility in that disease state or disorder. In numerous cases where the tissue/cell source is a library, column 7 identifies the vector used to generate the library.

[31] Table 5 provides a key to the OMIM reference identification numbers disclosed in Table 1A, column 10. OMIM reference identification numbers (Column 1) were derived from Online Mendelian Inheritance in Man (Online Mendelian Inheritance in Man, OMIM.

McKusick-Nathans Institute for Genetic Medicine, Johns Hopkins University (Baltimore, MD) and National Center for Biotechnology Information, National Library of Medicine, (Bethesda, MD) 2000. World Wide Web URL: <http://www.ncbi.nlm.nih.gov/omim/>). Column 2 provides diseases associated with the cytologic band disclosed in Table 1A, column 9, as determined using the Morbid Map database.

[32] Table 6 summarizes ATCC Deposits, Deposit dates, and ATCC designation numbers of deposits made with the ATCC in connection with the present application.

[33] Table 7 shows the cDNA libraries sequenced, and ATCC designation numbers and vector information relating to these cDNA libraries.

[34] Table 8 provides a physical characterization of clones encompassed by the invention. The first column provides the unique clone identifier, "Clone ID NO:Z", for certain cDNA clones of the invention, as described in Table 1A. The second column provides the size of the cDNA insert contained in the corresponding cDNA clone.

Definitions

[35] The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

[36] In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide. The term "isolated" does not refer to genomic or cDNA libraries, whole cell total or mRNA preparations, genomic DNA preparations (including those separated by electrophoresis and transferred onto blots), sheared whole cell genomic DNA preparations or other compositions where the art demonstrates no distinguishing features of the polynucleotide/sequences of the present invention.

[37] As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence encoding SEQ ID NO:Y or a fragment or variant thereof; a nucleic acid sequence contained in SEQ ID NO:X (as described in column 3 of Table 1A) or the complement thereof; a cDNA sequence contained in Clone ID NO:Z (as described in column 2 of Table 1A and contained within a library deposited with the ATCC); a nucleotide sequence encoding

the polypeptide encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B or a fragment or variant thereof; or a nucleotide coding sequence in SEQ ID NO:B as defined in column 6 of Table 1B or the complement thereof. For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having an amino acid sequence encoded by a polynucleotide of the invention as broadly defined (obviously excluding poly-Phenylalanine or poly-Lysine peptide sequences which result from translation of a polyA tail of a sequence corresponding to a cDNA).

[38] In the present invention, "SEQ ID NO:X" was often generated by overlapping sequences contained in multiple clones (contig analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X is deposited at Human Genome Sciences, Inc. (HGS) in a catalogued and archived library. As shown, for example, in column 2 of Table 1A, each clone is identified by a cDNA Clone ID (identifier generally referred to herein as Clone ID NO:Z). Each Clone ID is unique to an individual clone and the Clone ID is all the information needed to retrieve a given clone from the HGS library. Furthermore, certain clones disclosed in this application have been deposited with the ATCC on October 5, 2000, having the ATCC designation numbers PTA 2574 and PTA 2575; and on January 5, 2001, having the depositor reference numbers TS-1, TS-2, AC-1, and AC-2. In addition to the individual cDNA clone deposits, most of the cDNA libraries from which the clones were derived were deposited at the American Type Culture Collection (hereinafter "ATCC"). Table 7 provides a list of the deposited cDNA libraries. One can use the Clone ID NO:Z to determine the library source by reference to Tables 6 and 7. Table 7 lists the deposited cDNA libraries by name and links each library to an ATCC Deposit. Library names contain four characters, for example, "HTWE." The name of a cDNA clone (Clone ID) isolated from that library begins with the same four characters, for example "HTWEP07". As mentioned below, Table 1A correlates the Clone ID names with SEQ ID NO:X. Thus, starting with an SEQ ID NO:X, one can use Tables 1, 6 and 7 to determine the corresponding Clone ID, which library it came from and which ATCC deposit the library is contained in. Furthermore, it is possible to retrieve a given cDNA clone from the source library by techniques known in the art and described elsewhere herein. The ATCC is located at 10801 University Boulevard, Manassas, Virginia 20110-2209, USA. The ATCC deposits were made pursuant to the terms

of the Budapest Treaty on the international recognition of the deposit of microorganisms for the purposes of patent procedure.

[39] In specific embodiments, the polynucleotides of the invention are at least 15, at least 30, at least 50, at least 100, at least 125, at least 500, or at least 1000 continuous nucleotides but are less than or equal to 300 kb, 200 kb, 100 kb, 50 kb, 15 kb, 10 kb, 7.5kb, 5 kb, 2.5 kb, 2.0 kb, or 1 kb, in length. In a further embodiment, polynucleotides of the invention comprise a portion of the coding sequences, as disclosed herein, but do not comprise all or a portion of any intron. In another embodiment, the polynucleotides comprising coding sequences do not contain coding sequences of a genomic flanking gene (i.e., 5' or 3' to the gene of interest in the genome). In other embodiments, the polynucleotides of the invention do not contain the coding sequence of more than 1000, 500, 250, 100, 50, 25, 20, 15, 10, 5, 4, 3, 2, or 1 genomic flanking gene(s).

[40] A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained in SEQ ID NO:X, or the complement thereof (e.g., the complement of any one, two, three, four, or more of the polynucleotide fragments described herein), the polynucleotide sequence delineated in columns 8 and 9 of Table 2 or the complement thereof, and/or cDNA sequences contained in Clone ID NO:Z (e.g., the complement of any one, two, three, four, or more of the polynucleotide fragments, or the cDNA clone within the pool of cDNA clones deposited with the ATCC, described herein), and/or the polynucleotide sequence delineated in column 6 of Table 1B or the complement thereof. "Stringent hybridization conditions" refers to an overnight incubation at 42 degree C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65 degree C.

[41] Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37 degree C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH₂PO₄; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 ug/ml salmon sperm blocking DNA; followed by washes at 50 degree C with 1XSSPE, 0.1% SDS.

In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

[42] Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

[43] Of course, a polynucleotide which hybridizes only to polyA⁺ sequences (such as any 3' terminal polyA⁺ tract of a cDNA shown in the sequence listing), or to a complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone generated using oligo dT as a primer).

[44] The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

[45] The polypeptide of the present invention can be composed of amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous

research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth. Enzymol. 182:626-646 (1990); Rattan et al., Ann. N.Y. Acad. Sci. 663:48-62 (1992)).

[46] "SEQ ID NO:X" refers to a polynucleotide sequence described, for example, in Tables 1A or 2, while "SEQ ID NO:Y" refers to a polypeptide sequence described in column 6 of Table 1A. SEQ ID NO:X is identified by an integer specified in column 4 of Table 1A. The polypeptide sequence SEQ ID NO:Y is a translated open reading frame (ORF) encoded by polynucleotide SEQ ID NO:X. "Clone ID NO:Z" refers to a cDNA clone described in column 2 of Table 1A.

[47] "A polypeptide having functional activity" refers to a polypeptide capable of displaying one or more known functional activities associated with a full-length (complete) protein. Such functional activities include, but are not limited to, biological activity, antigenicity [ability to bind (or compete with a polypeptide for binding) to an anti-polypeptide antibody], immunogenicity (ability to generate antibody which binds to a

specific polypeptide of the invention), ability to form multimers with polypeptides of the invention, and ability to bind to a receptor or ligand for a polypeptide.

[48] The polypeptides of the invention can be assayed for functional activity (e.g. biological activity) using or routinely modifying assays known in the art, as well as assays described herein. Specifically, one of skill in the art may routinely assay signal transduction pathway component polypeptides (including fragments and variants) of the invention for activity using assays as described in Examples 38, 39, 49, 52-57, 64 and 67.

[49] "A polypeptide having biological activity" refers to a polypeptide exhibiting activity similar to, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention).

[50] Table 1A summarizes some of the polynucleotides encompassed by the invention (including contig sequences (SEQ ID NO:X) and clones (Clone ID NO:Z) and further summarizes certain characteristics of these polynucleotides and the polypeptides encoded thereby.

Polynucleotides and Polypeptides of the Invention

TABLE 1A

Gene No:	Clone ID NO: Z	Contig ID:	SEQ ID NO: X	ORF (From-To)	AA SEQ ID NO: Y	Predicted Epitopes	Tissue Distribution Library code: count (see Table IV for Library Codes)	Cytologic Band	OMIM Disease Reference(s):
1	HDPTE21	1165861	11	33 - 1790	624	Pro-16 to Gln-22,	AR051: 26, AR050: 22, AR054: 21, AR089: 1, AR061: 1 H0529: 4, L0770: 4, L0748: 4, L0749: 3, L0777: 3, S0036: 2, L0756: 2, S0360: 1, H0036: 1, H0318: 1, H0457: 1, H0051: 1, H0328: 1, H0644: 1, S0002: 1, L0761: 1, L0766: 1, L0804: 1, L0784: 1, H0521: 1 and L0759: 1.		
						Arg-34 to Asn-41,			
						Arg-49 to Lys-55,			
						Leu-156 to Thr-163,			
2	H6EDR51	1197894	12	1 - 1935	625	Glu-169 to Glu-174,			
						Ser-198 to Glu-214,			
						Glu-246 to Pro-252,			
						Arg-260 to Ser-271,			
						Val-286 to Gly-291,			
						Ser-304 to Glu-335,			
						Pro-436 to Pro-451,			
						Ser-482 to Gly-487,			
						Val-498 to Ser-505,			
						Asp-564 to Lys-585.			
						Gly-26 to Gly-32.			
						Glu-35 to Gln-44,	AR089: 1, AR061: 1 L0794: 11, L0777: 9,		
						Arg-70 to Val-77,			

H0255: 4, H0559: 4,
H0486: 3, H0581: 3,
L0809: 3, H0521: 3,
S0404: 3, H0556: 2,
H0580: 2, H0635: 2,
H0271: 2, H0135: 2,
H0703: 2, L0748: 2,
L0758: 2, H0543: 2,
H0422: 2, H0265: 1,
H0583: 1, H0656: 1,
H0638: 1, S0354: 1,
S0360: 1, H0637: 1,
H0600: 1, H0592: 1,
H0586: 1, H0587: 1,
H0257: 1, H0069: 1,
H0253: 1, S0049: 1,
H0199: 1, S0368: 1,
H0212: 1, H0494: 1,
H0529: 1, L0763: 1,
L0637: 1, L0761: 1,
L0630: 1, L0764: 1,
L0648: 1, L0768: 1,
L0766: 1, L0378: 1,
L0806: 1, L0655: 1,
L0657: 1, L0659: 1,
L0789: 1, H0593: 1,

3	HAPRA41	1154054	13	2 - 1276	626	<p>Ser-5 to Arg-24, Trp-27 to Ala-32, Arg-48 to Gln-54, Lys-71 to Gln-79, Pro-93 to His-101, Lys-104 to Thr-110, Ser-119 to Gln-125, Val-141 to Pro-152, Leu-158 to Gly-171, Asn-183 to Ala-198, Gly-217 to Asp-233, Ser-244 to Asn-258, Lys-264 to Leu-269, Ser-310 to Gly-316,</p>	<p>930788</p> <p>445</p> <p>1 - 1248</p> <p>1058</p> <p>Glu-26 to Gln-35, Arg-61 to Val-68, Ala-104 to Gly-114, Ser-119 to Phe-124, Gly-226 to His-233, Glu-240 to Leu-245, Pro-277 to Arg-283.</p>	<p>H0670: 1, S0378: 1, S0152: 1, H0696: 1, H0134: 1, L0779: 1, H0445: 1, H0542: 1 and H0423: 1.</p> <p>AR061: 3, AR089: 2 L0777: 2, S0001: 1, S0222: 1, H0575: 1, H0618: 1, H0253: 1, H0266: 1, H0038: 1, H0616: 1, L0643: 1, L0352: 1 and L0758: 1.</p>		
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									L0774: 1, L0790: 1, L0663: 1, L0665: 1, H0345: 1, L0742: 1, L0748: 1, L0749: 1, H0707: 1, L0595: 1 and L0366: 1.			
6	HCE3E50	1227586	16	4 - 1650	629	Pro-1 to Ser-10, Pro-24 to Ser-29, Pro-43 to Glu-61.			AR061: 1, AR089: 1 H0521: 14, L0439: 6, L0754: 6, L0794: 4, L0748: 4, S0278: 3, L0766: 3, L0751: 3, L0747: 3, L0749: 3, H0556: 2, H0486: 2, H0250: 2, H0179: 2, H0271: 2, S0002: 2, S0426: 2, L0770: 2, L0769: 2, L0775: 2, L0659: 2, L0411: 1, S0134: 1, H0638: 1, S0418: 1, S0420: 1, S0354: 1, S0358: 1, S0360: 1, S0222: 1, H0613: 1, H0052: 1, H0051: 1, L0143: 1, L0455: 1, H0124: 1, H0090: 1, H0551: 1.			

9	HDPLT89	962403	19	83 - 931	632	<p>Tyr-73 to Gly-85, Ala-98 to Ala-104, Ser-115 to Asp-124, Gly-189 to Gly-194, Pro-199 to Leu-204, Ala-214 to Asp-225, Thr-260 to Gln-268, Pro-279 to Ser-284.</p>	<p>H0657: 2, H0553: 2, L0632: 2, L0748: 2, H0445: 2, L0605: 2, H0422: 2, H0265: 1, H0556: 1, S0114: 1, H0583: 1, H0650: 1, S0116: 1, H0341: 1, S0360: 1, H0676: 1, H0497: 1, H0486: 1, H0075: 1, H0581: 1, H0421: 1, S0388: 1, H0271: 1, H0031: 1, H0090: 1, H0591: 1, H0038: 1, L0638: 1, L0667: 1, L0363: 1, L0774: 1, L0775: 1, L0658: 1, L0659: 1, L0809: 1, L0647: 1, L0790: 1, H0701: 1, H0658: 1, H0555: 1, L0779: 1, L0777: 1, L0731: 1 and H0423: 1.</p>	<p>AR054: 57, AR051: 36, AR050: 36, AR089: 4, AR061: 1 L0731: 19, L0766: 16,</p>	
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Lys-170 to Gly-179, Thr-183 to Trp-188, Arg-193 to Glu-206, Asp-222 to Val-228, Ser-262 to Ser-277.	H0521: 11, L0748: 7, L0754: 7, L0806: 6, L0749: 6, L0794: 5, L0666: 5, S0360: 4, L0663: 4, L0740: 4, L0747: 4, H0656: 3, L0771: 3, L0662: 3, L0774: 3, L0665: 3, L0439: 3, L0777: 3, L0755: 3, H0638: 2, H0431: 2, H0620: 2, H0494: 2, S0002: 2, L0769: 2, L0803: 2, L0438: 2, H0689: 2, H0659: 2, H0658: 2, H0518: 2, S0206: 2, L0750: 2, S0242: 2, H0423: 2, H0650: 1, H0341: 1, H0661: 1, H0662: 1, H0300: 1, S0418: 1, S0376: 1, H0580: 1, S0045: 1, L0717: 1, H0453: 1, H0370: 1, H0497: 1, H0574: 1, H0632: 1, H0486: 1, L0021: 1,
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[illegible]

10	HDPSU48	1228284	20	466 - 987	633	Gln-1 to Gly-8, Ile-15 to Asp-20; Lys-61 to Glu-69, Pro-93 to Lys-102, Ala-147 to Leu-156.	AR089: 1, AR061: 0 L0766: 10, L0803: 6, L0754: 5, S0152: 4, L0771: 3, H0656: 2, L0662: 2, L0774: 2.	AR089: 1, AR061: 0 L0766: 10, L0803: 6, L0754: 5, S0152: 4, L0771: 3, H0656: 2, L0662: 2, L0774: 2.	AR089: 1, AR061: 0 L0766: 10, L0803: 6, L0754: 5, S0152: 4, L0771: 3, H0656: 2, L0662: 2, L0774: 2.
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[illegible]

					Pro-159 to Asp-174.	S0380: 2, H0423: 2, H0624: 1, H0685: 1, L0002: 1, H0583: 1, L0760: 1, H0661: 1, S0358: 1, S0360: 1, H0637: 1, H0601: 1, H0486: 1, H0457: 1, H0247: 1, S0003: 1, T0067: 1, S0002: 1, S0426: 1, H0529: 1, L0770: 1, L0764: 1, L0806: 1, L0655: 1, L0659: 1, L0666: 1, L0663: 1, L0664: 1, S0428: 1, S0126: 1, H0435: 1, H0521: 1, H0522: 1, L0747: 1, L0756: 1, L0759: 1, H0445: 1 and H0422: 1.

11	HDPWE80	909916	21	94 - 765	634	Pro-235 to Asp-250. Asp-8 to Cys-21, Val-25 to Asn-33, Thr-47 to Pro-55, Ala-62 to Thr-68, Val-79 to Lys-88, Asn-91 to Asn-104, Tyr-114 to Gly-120, Thr-187 to Glu-192, Ile-217 to Thr-224.	H0521: 9, L0595: 2, L0593: 1 and L0594: 1.			
12	HDQFY84	1092137	22	2 - 2776	635	Glu-94 to Tyr-102, Pro-105 to Asn-112, Thr-121 to Gly-137, Glu-157 to Gly-162, Glu-179 to Phe-186, Cys-211 to Thr-222, Ser-240 to Lys-245, Thr-262 to Asn-279, Arg-288 to Pro-306, Asn-332 to Gln-339, Ser-375 to Leu-382, Arg-408 to Gly-415, Asp-423 to Thr-428, Ser-471 to Asn-476, Pro-545 to Gly-551, Ser-606 to Pro-616,	AR051: 2, AR050: 1, AR061: 1, AR054: 1, AR089: 0 S0354: 8, H0254: 2, S0358: 2, H0580: 2, H0521: 2, H0656: 1, H0590: 1, H0457: 1, H0271: 1 and H0488: 1.			

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H0333: 2, H0012: 2, T0010: 2, H0252: 2, H0063: 2, H0059: 2, S0002: 2, L0775: 2, L0655: 2, L0663: 2, L0665: 2, H0593: 2, H0658: 2, H0539: 2, H0555: 2, L0743: 2, L0744: 2, L0752: 2, L0731: 2, H0543: 2, H0624: 1, H0265: 1, H0650: 1, H0656: 1, S0212: 1, H0306: 1, H0305: 1, S0360: 1, S0046: 1, H0619: 1, S0222: 1, S6014: 1, H0613: 1, H0492: 1, H0250: 1, H0635: 1, H0427: 1, L0021: 1, H0036: 1, H0421: 1, H0399: 1, H0416: 1, H0188: 1, S0250: 1, L0143: 1, H0617: 1, H0673: 1, H0124: 1, H0163: 1, H0634: 1, H0087: 1, T0067: 1,						
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16	HHBGJ53	926486	452	1 - 720	1065	Arg-16 to Trp-21, Asn-27 to Pro-35, Lys-116 to Glu-126, Glu-155 to Trp-164, Ser-193 to Val-198, Gly-217 to Arg-223.	H0264: 1, H0272: 1, H0412: 1, H0413: 1, H0100: 1, S0344: 1, S0426: 1, L0770: 1, L0638: 1, L0761: 1, L0794: 1, L0650: 1, L0661: 1, L0546: 1, S0053: 1, H0689: 1, H0521: 1, S014: 1, L0748: 1, L0740: 1, L0779: 1, L0780: 1, L0753: 1, L0759: 1, H0445: 1, H0595: 1, L0362: 1, H0653: 1 and H0506: 1.		
		1187668	26	312 - 1	639				
		909912	453	1 - 282	1066	Ser-1 to Ser-7, Ser-25 to Arg-31.			
						AR089: 8, AR061: 5 L0740: 2 and H0373: 1.			

17	HHFJF24	1212624	27	1374 - 538	640	1.	Lys-1 to Ala-6, Ser-38 to Gln-43.	AR089: 1, AR061: 0 S0001: 1, H0619: 1, H0586: 1, H0427: 1 and L0595: 1.		
18	HHFMM10	910065	454	3 - 206	1067					
		1178801	28	368 - 751	641	Ser-19 to Thr-29, Lys-62 to Arg-67, Gln-102 to Phe-113.	AR089: 20, AR061: 7 H0031: 2, H0619: 1 and S0036: 1.			
		962997	455	95 - 493	1068	Gly-1 to Ser-13, Ile-24 to Phe-29.				
19	HHPBA42	901921	29	1 - 912	642	Gly-9 to Gln-15.	AR061: 133, AR089: 118 L0764: 4, L0659: 4, L0761: 3, S0360: 2, H0031: 2, L0662: 2, L0747: 2, L0750: 2, H0624: 1, H0295: 1, S0356: 1, S0132: 1, H0351: 1, L0394: 1, L0738: 1, H0051: 1, H0328: 1, L0796: 1, L0646: 1, L0800: 1, L0794: 1, L0549: 1, L0803: 1, L0806: 1, L0809: 1, L0788: 1,			

									L0789: 1, S0374: 1, H0435: 1, H0539: 1, S0378: 1, S0146: 1, L0754: 1, L0780: 1, L0752: 1 and L0591: 1.			
20	HHPSP89	1217052	30	2 - 916	643	Gly-1 to Ile-11, Pro-49 to Asp-59, Val-64 to Leu-70, Gly-105 to Ser-112, Ser-130 to Ala-146, Asn-223 to Val-229, Asn-272 to Asp-278, Lys-294 to Tyr-305.			AR089: 1, AR061: 0 H0038: 3, H0616: 3, S0386: 2, L0366: 2, S0001: 1, S0360: 1, H0208: 1, S0046: 1, S6026: 1, H0486: 1, H0052: 1, H0201: 1, T0010: 1, S0036: 1, L0776: 1, S0216: 1, H0701: 1, H0593: 1, S0152: 1, H0521: 1, L0753: 1, L0758: 1 and S0031: 1.			
		910024	456	1 - 906	1069	Pro-46 to Asp-56, Val-61 to Leu-67, Gly-102 to Ser-109, Ser-127 to Ala-143, Asn-220 to Val-226.						
21	HKABX13	1167182	31	1 - 786	644	Lys-49 to Trp-55, Tyr-66 to Val-79, Arg-89 to Asp-106,			AR089: 12, AR061: 2 H0556: 1, H0250: 1, H0494: 1, L0809: 1 and			

[illegible]

					Gln-137 to Asn-142.	L0596: 1.		
	958656	457	2 - 763	1070	Pro-1 to Arg-15, Lys-49 to Trp-55, Tyr-66 to Val-79, Arg-89 to Asp-106, Gln-137 to Asn-142, Ala-171 to Tyr-178, Glu-224 to Ser-231.			
22	HLTHG77	1162409	32	2 - 406	645	Met-17 to Met-24, Ser-31 to Asp-37, Leu-70 to Asp-97.	AR089: 0, AR061: 0 S0192: 13, L0471: 4, H0051: 4, H0413: 4, L0779: 4, S0418: 3, S0388: 3, H0591: 3, L0666: 3, S0242: 3, S0414: 2, H0012: 2, H0040: 2, H0100: 2, S0422: 2, L0766: 2, L0663: 2, S0152: 2, L0748: 2, L0439: 2, L0591: 2, S0196: 2, H0170: 1, H0686: 1, S0134: 1, S0282: 1, S0356: 1, S0045: 1, S0222: 1, H0441: 1, H0587: 1, T0039: 1, H0263: 1 T0110: 1	

23	HLWBZ09	1179714	33	123 - 1349	646	Met-14 to Met-21, Ser-28 to Asp-34, Leu-67 to Asp-94, Ala-109 to Ile-123.	<p>H0050: 1, H0620: 1, H0266: 1, H0644: 1, L0055: 1, H0412: 1, H0494: 1, L0646: 1, L0662: 1, L0626: 1, L0768: 1, L0794: 1, L0375: 1, L0656: 1, H0547: 1, H0519: 1, H0672: 1, S0328: 1, H0134: 1, L0758: 1, S0031: 1, S0260: 1, L0608: 1, H0667: 1 and S0412: 1.</p> <p>AR089: 5, AR061: 3 L0748: 6, L0754: 4, L0775: 3, S0206: 3, L0758: 3, H0543: 3, H0309: 2, H0553: 2, H0644: 2, L0779: 2, L0752: 2, L0485: 2, L0600: 2, H0638: 1, S0356: 1, H0580: 1,</p>		
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24	HLWEH54	1227713	459	112 - 477	1072	Lys-211 to Phe-218, Ser-230 to Pro-236, Ala-276 to Glu-281, Arg-297 to His-316, Ser-330 to Ser-335, Ser-367 to Thr-376, Pro-383 to Cys-394.	S0046: 1, L0717: 1, S0222: 1, H0635: 1, H0575: 1, S0010: 1, S6028: 1, S0316: 1, L0483: 1, H0032: 1, S0036: 1, H0038: 1, H0040: 1, H0623: 1, T0041: 1, H0494: 1, L0763: 1, L0774: 1, L0805: 1, L0776: 1, L0663: 1, H0519: 1, S0044: 1, H0436: 1, S0032: 1, L0744: 1, L0740: 1, L0747: 1, L0750: 1, L0757: 1, L0604: 1 and S0276: 1.		
						Val-9 to Arg-14, Glu-22 to Phe-30. Asn-38 to Tyr-46, Pro-56 to Asp-71, Asn-84 to Cys-96, Ser-110 to Val-142, Arg-181 to Leu-187, His-193 to Gly-198, Thr-201 to Arg-210, Asn-224 to Leu-230,	AR061: 0, AR089: 0 S0414: 12, L0740: 12, L0803: 9, L0438: 8, L0439: 6, L0756: 6, L0591: 6, H0623: 5, L0595: 5, L0769: 4, S0045: 3, S0046: 3, H0031: 3, L0771: 3,		

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Thr-246 to Gly-251, Ser-267 to Ser-272, Ser-284 to Gln-290, Asp-294 to Asn-301, Asp-318 to Asn-324, Asn-338 to Glu-343, Gln-353 to Glu-362, Lys-374 to Lys-381, Asn-397 to Ala-409, Pro-426 to Tyr-436, Thr-469 to Pro-474, Ile-486 to Asn-492, Ile-499 to Ile-505, Lys-531 to Gln-539, Lys-585 to His-592, Lys-627 to Gly-635.	H0648: 3, L0747: 3, L0749: 3, H0341: 2, S0420: 2, S0356: 2, S0354: 2, S0222: 2, H0013: 2, H0575: 2, L0738: 2, H0046: 2, S0051: 2, S0003: 2, H0551: 2, H0413: 2, H0056: 2, H0529: 2, L0768: 2, L0794: 2, L0666: 2, H0547: 2, L0750: 2, L0779: 2, L0758: 2, L0686: 2, L0593: 2, S0412: 2, H0170: 1, L0441: 1, H0685: 1, H0381: 1, H0305: 1, S0007: 1, H0619: 1, S6026: 1, H0549: 1, H0550: 1, S6014: 1, H0586: 1, H0333: 1, H0559: 1, T0039: 1, H0156: 1, H0098: 1, H0036: 1, H0505: 1, H0327: 1, S0050: 1, H0051: 1, S0388: 1, T0010: 1,
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27	HMCFB47					Asp-96 to Pro-102, Pro-117 to Gly-124, Pro-132 to Ser-143.	AR089: 31, AR061: 30 H0341: 1, H0050: 1, S0344: 1, L0750: 1 and L0366: 1.		
		1151498	37	808 - 275	650	Arg-23 to Thr-29, Gly-45 to Arg-51, Pro-56 to Glu-66.			
		910088	463	1 - 393	1076	Arg-8 to Pro-15, Gly-37 to Arg-46, Lys-59 to Leu-67, Ala-108 to Asp-113.			
28	HMSOI20	1178817	38	417 - 2222	651	Arg-10 to His-17, Gln-24 to Asn-29, Glu-42 to His-51, Glu-63 to Asp-70, His-78 to Arg-84, Lys-101 to Phe-106, Phe-171 to Ser-180, Lys-182 to Gln-189, Pro-191 to Thr-197, Glu-236 to Ala-241, Gly-250 to Asn-256, Ser-293 to Ser-301, Lys-320 to Leu-325, Glu-334 to Val-340, Asp-453 to Gly-466,	AR061: 1, AR089: 0 L0748: 2, S0001: 1, H0575: 1, S0038: 1, S0426: 1, H0521: 1 and L0751: 1.		

						Pro-473 to Asp-478, Leu-576 to Lys-585.				
	928168	464	1 - 465	1077		Tyr-114 to Trp-119, Gln-124 to Ile-129.				
29	HOENH55	1163460	39	1 - 624	652	Asp-1 to Arg-7, Glu-19 to Leu-32, Leu-36 to Ser-49, Ser-74 to Pro-100, Ser-113 to Val-130, Thr-143 to His-154, Gln-161 to Arg-167, Val-194 to Phe-200.	AR061: 0, AR089: 0 S0126: 2, S0046: 1, H0645: 1, H0550: 1 and H0135: 1.			
	922141	465	1 - 624	1078		Asp-1 to Arg-7, Glu-19 to Leu-32, Leu-36 to Ser-49, Ser-74 to Pro-100, Ser-113 to Val-130, Thr-143 to His-154, Gln-161 to Arg-167, Val-194 to Phe-200.				
30	HPIA101	1078178	40	794 - 321	653	Cys-52 to Trp-57, Pro-69 to Asp-74, Glu-95 to Ser-115, Pro-136 to Gly-143.	AR050: 204, AR054: 168, AR051: 151, AR089: 9, AR061: 6 S0140: 2, L0783: 2, S0150: 1, L0769: 1, L0774: 1, L0775: 1,			

31	HPJCT50	909928	466	288 - 764	1079	Glu-48 to Leu-53.	L0809: 1, H0648: 1 and L0748: 1.		
		1201773	41	32 - 1567	654	Ser-3 to Trp-9, Arg-12 to Ser-18, Asp-42 to Gln-53, Arg-79 to Gly-90, Val-103 to Asp-108, Gly-175 to Asn-193, Ser-210 to Thr-217, Lys-242 to Glu-251, Glu-267 to Lys-273, Leu-287 to Lys-293, Ser-311 to Glu-318, Pro-335 to Lys-364, Asn-370 to Glu-376, Ala-392 to Thr-401.	AR089: 6, AR061: 4 H0561: 2, S0002: 2, H0521: 2, H0522: 2, H0656: 1, H0341: 1, H0550: 1, T0040: 1, H0036: 1, H0031: 1, H0560: 1, S0152: 1 and H0134: 1.		
		919836	467	32 - 1567	1080	Ser-3 to Trp-9, Arg-12 to Ser-18, Asp-42 to Gln-53, Arg-79 to Gly-90, Val-103 to Asp-108, Gly-175 to Asn-193, Ser-210 to Thr-217, Lys-242 to Glu-251, Glu-267 to Lys-273,			

32	HPMFE91	1164740	42	605 - 1813	655	Leu-287 to Lys-293, Ser-311 to Glu-318, Pro-335 to Lys-364, Asn-370 to Glu-376, Ala-392 to Thr-401. Glu-6 to Asp-20, Thr-25 to Lys-31, Lys-73 to Ala-95, Glu-102 to Phe-109, Pro-112 to Pro-118, Asp-136 to Leu-152, Val-246 to Thr-253, Thr-298 to Glu-303, Val-312 to Arg-322, Pro-341 to Arg-349, Lys-378 to Phe-388, Val-392 to Ala-397.	AR061: 3, AR089: 2 L0766: 10, L0752: 8, L0439: 6, L0747: 6, L0740: 5, L0756: 5, L0779: 4, L0777: 4, L0731: 4, S0051: 3, L0803: 3, L0774: 3, L0754: 3, S0360: 2, H0574: 2, L0763: 2, L0805: 2, L0809: 2, L0663: 2, L0751: 2, L0755: 2, L0759: 2, L0601: 2, H0624: 1, S0040: 1, S0298: 1, S0420: 1, H0580: 1, H0351: 1, H0600: 1, H0331: 1, H0013: 1, L0021: 1, H0575: 1, H0590: 1, T0110: 1, H0012: 1, H0615: 1, H0031: 1, H0553: 1,		
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						H0591: 1, H0646: 1, S0002: 1, L0772: 1, L0645: 1, L0773: 1, L0662: 1, L0794: 1, L0381: 1, L0775: 1, L0776: 1, L0657: 1, L0659: 1, L0528: 1, L0790: 1, L0666: 1, H0547: 1, H0648: 1, H0539: 1, S0152: 1, H0696: 1, S0044: 1, S0028: 1, L0758: 1, L0366: 1, S0011: 1, S0276: 1, H0422: 1 and S0424: 1.		
33	HRAED51	910026	468	98 - 955	1081	Pro-25 to Arg-32, Met-56 to Ser-75, Asn-90 to Trp-95, Lys-111 to Arg-121, His-134 to Arg-140, Arg-153 to Gln-162, Gln-169 to Gly-186. Phe-16 to Asp-22, Val-93 to Gly-98. Pro-6 to Arg-12.	AR089: 4, AR061: 2 S0212: 1 and H0555: 1.	
34	HSMBA19	909859	469	55 - 627	1082	Leu-9 to Gln-17,	AR089: 4, AR061: 1	

35	HSYCY88	914775	45	448 - 1089	658	Leu-48 to Ser-55, Ser-63 to Ser-71, Asn-76 to Ala-82, Ser-87 to Phe-99, His-125 to Gly-140, Pro-160 to Asp-165.	AR089: 2, AR061: 2 L0751: 11, L0747: 7, H0009: 5, L0659: 5, L0731: 5, S0046: 4, L0663: 4, H0392: 3, H0024: 3, H0124: 3, H0135: 3, L0500: 3, L0662: 3, L0508: 3, L0493: 3, L0779: 3, L0777: 3, L0758: 3, L0759: 3, S0360: 2, S0007: 2, H0208: 2, H0486: 2, H0012: 2, H0620: 2, H0264: 2, L0770: 2, L0769: 2, L0648: 2, L0775: 2, L0438: 2, L0744: 2, L0439: 2, L0749: 2, L0756: 2, S0260: 2, H0171: 1, S0040: 1,		
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	S0420: 1, S0354: 1, S0045: 1, H0619: 1, H0549: 1, H0550: 1, H0592: 1, H0643: 1, H0427: 1, H0002: 1, H0599: 1, H0042: 1, H0575: 1, H0036: 1, H0590: 1, H0004: 1, H0618: 1, S0049: 1, H0597: 1, H0327: 1, H0150: 1, H0041: 1, L0471: 1, H0014: 1, H0051: 1, S6028: 1, S0250: 1, H0428: 1, H0622: 1, H0553: 1, H0644: 1, S0364: 1, H0551: 1, H0100: 1, S0112: 1, L0520: 1, L0502: 1, L0796: 1, L0771: 1, L0768: 1, L0497: 1, L0774: 1, L0378: 1, L0509: 1, L0776: 1, L0527: 1, L0515: 1, L0658: 1, L0809: 1, L0647: 1, L0790: 1, L0791: 1,					
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									L0792: 1, L0666: 1, L0664: 1, L0665: 1, H0520: 1, H0547: 1, H0519: 1, S0126: 1, H0690: 1, H0658: 1, H0672: 1, H0651: 1, S0378: 1, S0380: 1, H0521: 1, S0037: 1, S0028: 1, L0743: 1, L0740: 1, L0750: 1 and L0757: 1.			
36	HTEDW26	909749	46	3 - 959	659				AR061: 9, AR089: 9 H0521: 2, L0758: 2, H0038: 1, L0644: 1, L0645: 1, L0764: 1, L0662: 1, L0794: 1, L0557: 1, L0747: 1 and L0779: 1.			
37	HTEKD92	1090524	47	263 - 1165	660			Asn-11 to Pro-18, Tyr-31 to Asp-36, Asp-98 to Ser-119, Asp-142 to Glu-155, Gly-215 to Ile-226, Ser-237 to Ser-251, Leu-255 to Arg-260, His-263 to Asn-270,	AR089: 1, AR061: 1 L0805: 11, L0779: 7, L0803: 5, L0789: 5, L0776: 4, L0794: 3, L0777: 3, H0575: 2, H0687: 2, S0003: 2, S0214: 2, L0766: 2, L0747: 2, L0731: 2,			

					Lys-287 to Thr-295.	H0662: 1, S0354: 1, H0549: 1, S0665: 1, T0048: 1, L0157: 1, H0031: 1, H0038: 1, S0002: 1, L0761: 1, L0800: 1, L0806: 1, L0787: 1, H0660: 1, S0330: 1, L0602: 1, S0206: 1, L0745: 1, L0756: 1, L0752: 1, L0759: 1, L0591: 1 and H0543: 1.		
910027	471	249 - 1151	1084	Asn-11 to Pro-18, Tyr-31 to Asp-36, Asp-98 to Ser-119, Asp-142 to Glu-155, Gly-215 to Ile-226, Ser-237 to Ser-251, Leu-255 to Arg-260, His-263 to Asn-270, Lys-287 to Thr-295.				
HTLDT05	1227127	48	625 - 2685	661	Trp-3 to Thr-14, Ala-21 to Arg-30, Glu-66 to Pro-74, Pro-103 to Gly-108, Ile-135 to Ile-142	AR089: 11, AR061: 7 H0253: 2, L0439: 1 and L0599: 1.		
38								

The figure consists of ten vertically stacked histograms, labeled \$k=1\$ through \$k=10\$. Each histogram shows the frequency of the number of non-zero elements in the vector \$\mathbf{x}_k\$. The x-axis for all plots ranges from approximately 80 to 180, with major ticks at 100 and 150. The y-axis represents frequency, ranging from 0 to 10. The distributions are roughly bell-shaped and centered around 120-130 non-zero elements.

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							H0576: 1, S0028: 1, L0747: 1, L0750: 1, L0755: 1, L0581: 1, S0242: 1 and S0196: 1.		
40	HTPHM71	1194698	50	1 - 1836	663	1086	Gly-9 to Thr-14, Lys-37 to Arg-42, Asp-47 to Ser-54, Asp-58 to Lys-63, Lys-82 to Asn-89. Tyr-17 to Val-23, Ala-54 to Leu-65, Arg-115 to Asn-120, Ser-150 to Ser-158, Glu-234 to Ile-251, His-272 to Asn-277, Gly-284 to Gln-303, Glu-327 to Lys-332, Thr-362 to Leu-368, Leu-390 to Asn-399, Ser-432 to Tyr-444, Asn-456 to Thr-467, Ser-474 to Thr-484, Asn-505 to Leu-510, Gln-563 to Ser-568, Ala-575 to Cys-582.	AR061: 4, AR089: 2 L0748: 8, H0040: 5, H0039: 3, L0766: 3, H0663: 2, T0040: 2, L0659: 2, L0754: 2, L0756: 2, H0556: 1, H0583: 1, H0650: 1, H0013: 1, H0318: 1, H0194: 1, H0596: 1, H0545: 1, S0003: 1, H0622: 1, H0634: 1, H0641: 1, H0647: 1, L0643: 1, L0794: 1, L0803: 1, S0052: 1, H0520: 1, H0539: 1, H0555: 1 and L0595: 1.	
		529764	473	66 - 461					
		909878	474	3 - 1094	1087		Tyr-14 to Phe-24.		

						4.			
41	HUUAR12	1194702	51	1 - 975	664	Pro-1 to Gln-11, Leu-36 to Gln-42, Glu-81 to Trp-86, Arg-108 to Lys-113, Arg-143 to Asn-149, Glu-154 to Asp-160, Glu-169 to His-174, Trp-184 to Ser-189, Lys-210 to Trp-217, Lys-233 to Tyr-239, Asp-308 to Gly-315.	AR089: 1, AR061: 1 L0809: 9, L0775: 3, L0758: 3, S0376: 2, L0439: 2, L0752: 2, H0656: 1, H0661: 1, H0586: 1, H0590: 1, H0594: 1, L0769: 1, L0761: 1, L0800: 1, L0662: 1, L0766: 1, L0803: 1, L0651: 1, L0805: 1, L0659: 1, L0788: 1, L0666: 1, L0779: 1 and S0276: 1.		
		944393	475	3 - 716	1088				
42	HWAGP22	1150195	52	310 - 1713	665	Gly-8 to Gly-15, Ser-25 to Ser-30, Glu-65 to Ala-71.	AR089: 1, AR061: 1 L0751: 7, H0575: 2, H0617: 2, H0634: 2, L0438: 2, L0747: 2, L0601: 2, H0556: 1, S0040: 1, H0484: 1, H0306: 1, S0360: 1, H0550: 1, H0607: 1, H0586: 1, H0004: 1, H0581: 1, H0288: 1, H0553: 1, H0100: 1,		

									T0042: 1, L0764: 1, L0766: 1, L0653: 1, S0052: 1, H0144: 1, H0701: 1, L0777: 1, S0192: 1, H0542: 1 and H0543: 1.		
	909919	476	3 - 1151	1089	Arg-15 to Leu-23, Glu-70 to Lys-76, Lys-96 to Gln-102, Leu-119 to Arg-124, Ala-141 to Glu-146, Leu-159 to Glu-169, Thr-195 to Lys-202, Gln-239 to Gly-251.						
43	HWBCE37	906968	53	3 - 431	666				AR089: 1, AR061: 0 H0580: 1 and H0427: 1.		
44	HWLFB60	1223499	54	2 - 2233	667	Gly-1 to Lys-8, Arg-52 to Gly-57, Asp-69 to Ser-74, Arg-90 to Lys-97, Asp-126 to Thr-132, Cys-155 to Thr-171, Lys-189 to Ala-198, Lys-239 to Ser-245, Gln-260 to Ser-276,			AR089: 6, AR061: 0 L0766: 4, L0666: 4, L0439: 4, S0354: 3, H0014: 3, H0551: 3, H0529: 3, L0665: 3, H0519: 3, L0740: 3, L0759: 3, H0656: 2, S0003: 2, H0553: 2, L0775: 2, L0657: 2,		

[illegible]

							Lys-1 to Thr-7, Arg-34 to Pro-41.		L0752: 2, L0755: 2, H0590: 1, H0014: 1, S0250: 1, L0772: 1, L0764: 1, L0804: 1, H0522: 1, S0406: 1, L0754: 1, L0779: 1, L0731: 1 and L0758: 1.	
47	HE6BK63	949702	479	551 - 339	1092	670	Gly-2 to Asp-11, Ser-71 to Gln-78, Ser-110 to Asn-117, Ser-155 to Ser-162, Thr-171 to Asp-181, Arg-193 to Leu-203, Arg-207 to Thr-215, Ala-225 to Lys-246, Lys-248 to Leu-255.		AR054: 21, AR050: 18, AR089: 17, AR051: 17, AR061: 14 H0090: 2, H0100: 2, L0792: 2, H0052: 1, H0012: 1, H0212: 1, S0426: 1, L0800: 1, L0663: 1, L0743: 1, L0756: 1 and L0780: 1.	
		661045	480	586 - 1191	1093		Ser-12 to Gln-19, Ser-51 to Asn-58, Ser-96 to Ser-103, Thr-112 to Asp-122, Arg-134 to Leu-144, Arg-148 to Thr-156, Ala-166 to Lys-187, Lys-189 to Gly-200.			

	L0754: 2, L0749: 2, L0777: 2, L0755: 2, L0758: 2, L0485: 2, S0242: 2, H0624: 1, H0170: 1, H0171: 1, H0295: 1, H0294: 1, S0134: 1, H0254: 1, H0662: 1, S0418: 1, S0420: 1, S0360: 1, H0675: 1, H0580: 1, S0045: 1, S0132: 1, H0619: 1, S0222: 1, H0370: 1, H0486: 1, N0009: 1, H0101: 1, H0250: 1, H0069: 1, H0635: 1, L0021: 1, H0318: 1, H0085: 1, H0544: 1, H0046: 1, H0024: 1, H0014: 1, L0163: 1, T0010: 1, H0594: 1, H0284: 1, H0673: 1, S0364: 1, H0135: 1, H0038: 1, H0379: 1, H0269: 1, H0059: 1, T0004: 1, L0351: 1, H0334: 1,	
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50	HAAAO58	909835	482	634 - 1146	1095	Pro-107 to Arg-120.	H0633: 1, S0144: 1, S0426: 1, L0639: 1, L0637: 1, L0761: 1, L0646: 1, L0644: 1, L0764: 1, L0766: 1, L0803: 1, L0775: 1, L0375: 1, L0652: 1, L0655: 1, L0384: 1, L0382: 1, L0663: 1, L0664: 1, L0665: 1, S0052: 1, H0144: 1, H0547: 1, L0741: 1, L0743: 1, L0740: 1, L0750: 1, H0595: 1, L0588: 1, L0601: 1, S0276: 1, H0423: 1, H0422: 1 and H0352: 1.		
		1091088	60	15 - 467	673	Arg-11 to Pro-17, Glu-43 to Gln-50, Gln-74 to Gln-85, Leu-127 to Asn-132, Arg-141 to Lys-146.			
		912622	483	15 - 467	1096	Arg-11 to Pro-17, Glu-43 to Gln-50,			
							AR089: 43, AR061: 8 H0592: 2, H0009: 1, H0030: 1, L0143: 1, H0264: 1, H0646: 1, L0653: 1, L0665: 1, S0052: 1 and H0658: 1.		

51	HADFK69	1091937	61	201 - 782	674	Gln-74 to Gln-85. Glu-1 to Gly-6, Glu-50 to Val-55, Tyr-62 to Leu-67, Glu-105 to Lys-113, Ser-127 to Val-132, Ala-141 to Val-146, Thr-154 to Leu-159, Leu-170 to Ser-177, Pro-182 to Asn-194.	AR089: 4, AR061: 1 L0794: 3, L0803: 3, L0809: 3, S0222: 2, L0747: 2, L0756: 2, L0752: 2, L0758: 2, H0171: 1, L0002: 1, S0420: 1, S6026: 1, H0427: 1, L0021: 1, H0051: 1, T0010: 1, H0032: 1, S0422: 1, L0775: 1, L0659: 1, L0367: 1, L0790: 1, L0666: 1, L0744: 1, L0754: 1, L0779: 1, L0777: 1 and L0757: 1.		
52	HDPMO62	912850 1152329	484 62	1 - 573 1 - 447	1097 675	Gly-38 to Pro-48, Pro-105 to Ser-116, Arg-120 to Ser-127, Ser-142 to Ser-149. Ala-14 to Gly-20, Gly-34 to Pro-44, His-128 to Ser-134.	AR089: 1 S0002: 2 and H0522: 1.		
53	HDPMO85	912722 1228282	485 63	1 - 582 138 - 719	1098 676	Glu-58 to Ala-72, Thr-91 to Gln-98.	AR089: 8, AR061: 2 L0759: 15, L0766: 9,		

						Glu-106 to Glu-115, Gln-128 to Asp-134, Lys-143 to Lys-148, Lys-170 to Ser-178, Ser-183 to Gly-190.	L0754: 8, L0769: 6, S0126: 6, L0439: 6, S0360: 5, L0776: 5, S0027: 5, L0731: 5, H0556: 4, H0341: 4, H0641: 4, L0747: 4, L0750: 4, L0596: 4, L0588: 4, H0650: 3, H0637: 3, H0013: 3, H0644: 3, H0412: 3, H0560: 3, L0809: 3, S0330: 3, H0521: 3, L0742: 3, H0543: 3, H0624: 2, H0171: 2, S0134: 2, H0656: 2, S0354: 2, S0007: 2, H0351: 2, H0333: 2, H0492: 2, H0599: 2, H0618: 2, H0581: 2, H0620: 2, S0051: 2, T0010: 2, H0594: 2, H0628: 2, H0090: 2, H0591: 2, H0264: 2, T0042: 2, L0641: 2, L0794: 2, L0774: 2, L0527: 2, L0659: 2,	
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912837	486	138 - 719	1099	Glu-51 to Val-56.	L0564: 1, H0022: 1, S0150: 1, H0633: 1, S0144: 1, L0770: 1, L0637: 1, L0761: 1, L0646: 1, L0764: 1, L0773: 1, L0662: 1, L0768: 1, L0381: 1, L0803: 1, L0775: 1, L0651: 1, L0653: 1, L0783: 1, L0789: 1, L0791: 1, L0792: 1, L0663: 1, S0428: 1, L0438: 1, H0547: 1, H0659: 1, H0658: 1, H0670: 1, H0672: 1, H0539: 1, H0518: 1, H0436: 1, S3014: 1, L0740: 1, L0751: 1, L0777: 1, L0780: 1, L0752: 1, L0755: 1, H0444: 1, H0445: 1, H0343: 1, L0592: 1, H0667: 1, H0136: 1, S0192: 1, S0194: 1, H0542: 1 and H0352: 1.
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54	HDPUY72	1228285	64	2 - 595	677	<p>Tyr-63 to Ala-72, Thr-91 to Gln-98, Glu-106 to Glu-115, Gln-128 to Asp-134, Lys-143 to Lys-148, Lys-170 to Ser-178, Ser-183 to Gly-190.</p> <p>Arg-1 to Pro-12, Pro-18 to Lys-25, Arg-28 to Cys-38, Val-61 to Leu-67, Pro-84 to Ser-95.</p>	<p>AR089: 7, AR061: 3 L0747: 17, L0439: 16, H0556: 12, L0731: 11, L0438: 10, L0740: 9, L0754: 8, L0596: 7, H0013: 6, L0659: 6, H0521: 6, S0278: 5, H0575: 5, S0126: 5, S3014: 5, L0755: 5, S0007: 4, S0003: 4, H0622: 4, H0673: 4, L0766: 4, L0803: 4, L0775: 4, L0666: 4, S0044: 4, L0748: 4, L0759: 4, L0599: 4, H0543: 4, S0358: 3, H0574: 3, H0178: 3, H0024: 3, H0051: 3, H0266: 3, S0214: 3,</p>		
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	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99
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	H0375: 1, H0594: 1, H0687: 1, H0553: 1, H0644: 1, L0055: 1, H0383: 1, H0169: 1, H0064: 1, H0708: 1, H0068: 1, H0598: 1, H0135: 1, H0038: 1, H0616: 1, H0413: 1, H0056: 1, S0112: 1, L0564: 1, H0280: 1, H0494: 1, H0625: 1, H0561: 1, S0344: 1, H0538: 1, L0763: 1, L0761: 1, L0772: 1, L0646: 1, L0800: 1, L0773: 1, L0662: 1, L0794: 1, L0650: 1, L0651: 1, L0806: 1, L0654: 1, L0528: 1, L0663: 1, H0144: 1, S0374: 1, H0520: 1, H0682: 1, H0659: 1, H0660: 1, H0648: 1, S0328: 1, S0330: 1, H0539: 1, S0380: 1, H0518: 1, S0146: 1,	
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								S0432: 1, S0390: 1, S0027: 1, L0750: 1, L0752: 1, L0757: 1, S0031: 1, H0445: 1, L0684: 1, L0592: 1, L0485: 1, L0608: 1, L0594: 1, S0026: 1, H0423: 1, H0422: 1, S0042: 1 and L0698: 1.		
55	HDTJF87	966153	487	1127 - 207	1100	Pro-1 to Pro-7, Pro-13 to Lys-20, Arg-23 to Cys-33, Val-56 to Leu-62, Pro-79 to Ser-90, Thr-169 to Gly-175, Thr-186 to Asn-192, Asp-200 to Pro-207, Lys-248 to Val-253, Lys-285 to Gly-292, Leu-294 to Cys-305.		AR089: 22, AR061: 3 H0486: 2, H0635: 1, H0052: 1, H0634: 1, L0748: 1 and H0444: 1.		
		1154640	65	24 - 497	678	Leu-4 to Thr-25, Thr-52 to Gln-57, Gly-111 to Ser-118, Pro-149 to Lys-158.				
		907527	488	14 - 412	1101	Leu-4 to Thr-25, Thr-52 to Gln-57				

56	HE8TB94	1178794	66	470 - 1087	679	Ser-95 to Gly-103, Thr-114 to Asn-120.	AR089: 2, AR061: 1 L0747: 10, H0266: 6, H0623: 6, L0740: 5, S0045: 3, H0050: 3, H0551: 3, L0777: 3, L0757: 3, L0759: 3, L0588: 3, H0056: 2, S0404: 2, L0745: 2, L0780: 2, L0589: 2, H0624: 1, H0170: 1, S0360: 1, H0329: 1, H0645: 1, H0437: 1, H0601: 1, H0486: 1, H0013: 1, H0123: 1, L0471: 1, H0328: 1, H0622: 1, H0591: 1, H0433: 1, H0413: 1, H0100: 1, S0210: 1, L0769: 1, L0659: 1, L0788: 1, S0126: 1, S0044: 1, S0146: 1, H0555: 1, S0037: 1, S0027: 1, L0748: 1, L0439: 1 and L0465: 1.		
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57	HE8UB55	935935	489	430 - 1104	1102	Cys-14 to Lys-31, Thr-87 to Leu-99, Arg-149 to Thr-154, Pro-208 to Ser-220. Glu-37 to Thr-42, Leu-127 to Glu-132, Ser-175 to Cys-183.	AR061: 2, AR089: 2 L0766: 3, H0556: 2, H0662: 2, S0420: 2, H0013: 2, H0457: 2, H0622: 2, L0659: 2, H0520: 2, S0152: 2, S0136: 2, H0521: 2, L0731: 2, H0624: 1, S0376: 1, S0132: 1, H0619: 1, L0021: 1, H0581: 1, H0251: 1, H0105: 1, H0373: 1, S0003: 1, H0328: 1, H0615: 1, H0553: 1, H0644: 1, H0628: 1, S0036: 1, H0551: 1, H0264: 1, H0623: 1, H0494: 1, S0144: 1, H0529: 1, L0783: 1, H0144: 1, S0126: 1, H0435: 1, S0328: 1, S0330: 1, H0539: 1,		
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58	HEBGA65	912932	1178633	68	309-977	681	1103	Glu-37 to Thr-42.	Lys-35 to Val-45, Ser-133 to Ala-138, Asp-162 to Asp-174, Gln-179 to Cys-186, Arg-214 to Pro-223.	AR089: 1, AR061: 0 L0748: 5, H0559: 3, H0009: 3, H0318: 2, H0581: 2, H0052: 2, H0135: 2, H0494: 2, L0770: 2, L0766: 2, L0809: 2, L0789: 2, L0439: 2, L0751: 2, L0755: 2, L0758: 2, L0604: 2, H0352: 2, S0040: 1, H0583: 1, H0671: 1, H0661: 1, H0402: 1, S0360: 1, S0007: 1, H0645: 1, H0351: 1, H0392: 1, H0587: 1, S0005: 1, H0156: 1, L0021: 1, H0545: 1, H0012: 1, H0024: 1, L0183: 1,		
										H0579: 1, S0454: 1, S0404: 1, L0745: 1, S0260: 1, H0445: 1, H0595: 1, S0026: 1, H0423: 1, H0422: 1 and H0506: 1.		

						T0010: 1, H0271: 1, H0188: 1, S0314: 1, H0252: 1, H0644: 1, H0316: 1, H0090: 1, H0551: 1, T0042: 1, H0625: 1, S0450: 1, S0426: 1, L0769: 1, L0637: 1, L0761: 1, L0667: 1, L0764: 1, L0771: 1, L0768: 1, L0774: 1, L0775: 1, L0806: 1, L0653: 1, L0776: 1, L0783: 1, L0545: 1, L0666: 1, S0428: 1, S0053: 1, S0216: 1, H0519: 1, H0682: 1, H0683: 1, H0658: 1, S0378: 1, H0518: 1, H0696: 1, H0478: 1, S0028: 1, L0747: 1, L0749: 1, L0750: 1, L0757: 1, L0759: 1, S0031: 1 and H0423: 1.					
912815	491	412 - 1035	1104	Ser-99 to Ala-104, Asp-128 to Asp-140.							

59	HEGBB59	1197907	69	398 - 1078	682	Thr-158 to Gly-163, Gly-195 to Tyr-201. Tyr-1 to Asp-11, Asp-64 to His-73, Ala-90 to Gly-100, Ile-133 to Asn-138, Val-195 to His-213.	AR061: 2, AR089: 2 L0731: 5, L0439: 4, H0662: 2, H0369: 2, L0105: 2, H0622: 2, L0794: 2, L0803: 2, L0804: 2, L0775: 2, L0809: 2, H0547: 2, L0754: 2, L0758: 2, L0485: 2, H0484: 1, S0360: 1, H0550: 1, H0441: 1, H0392: 1, H0031: 1, H0644: 1, L0369: 1, L0662: 1, L0768: 1, L0790: 1, L0663: 1, L0664: 1, S0126: 1, H0555: 1, L0756: 1, L0589: 1, L0592: 1, L0599: 1 and H0506: 1.			
		912601	492	265 - 645	1105	Tyr-1 to Asp-11, Asp-64 to His-73, Ala-90 to Ile-96.				
60	HELHC48	956003	70	816 - 403	683	Ile-3 to Thr-11, Asn-31 to Lys-40,	AR061: 2, AR089: 1 L0439: 22, L0770: 11,			

					Asn-44 to Val-53.	L0749: 11, S0003: 9, L0766: 8, L0754: 8, H0013: 7, L0665: 7, L0752: 7, L0731: 7, L0771: 6, L0775: 6, H0521: 6, S0356: 5, H0591: 5, L0438: 5, H0641: 4, L0776: 4, L0666: 4, L0663: 4, H0547: 4, H0519: 4, L0485: 4, H0556: 3, S0360: 3, S0045: 3, S0422: 3, L0598: 3, H0529: 3, L0659: 3, H0659: 3, L0755: 3, L0759: 3, L0595: 3, S0342: 2, S0212: 2, L0005: 2, S0358: 2, S0376: 2, S0222: 2, H0574: 2, H0575: 2, H0581: 2, H0046: 2, H0615: 2, H0428: 2, H0032: 2, H0316: 2, H0038: 2, L0769: 2, L0772: 2, L0649: 2, L0653: 2, L0518: 2,		
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					L0664: 2, H0144: 2, H0520: 2, S0126: 2, H0690: 2, S0152: 2, L0748: 2, L0780: 2, L0758: 2, S0260: 2, L0604: 2, L0601: 2, H0542: 2, H0422: 2, S0424: 2, H0624: 1, H0170: 1, T0049: 1, S0134: 1, H0650: 1, H0661: 1, H0638: 1, S0418: 1, S0354: 1, H0637: 1, H0580: 1, S0132: 1, H0645: 1, H0393: 1, L0717: 1, H0437: 1, H0549: 1, H0441: 1, H0431: 1, H0497: 1, H0486: 1, T0039: 1, H0156: 1, T0082: 1, H0590: 1, S0010: 1, H0505: 1, H0596: 1, L0040: 1, H0544: 1, H0545: 1, L0157: 1, H0050: 1, L0471: 1, H0024: 1, H0375: 1, H0687: 1.
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								L0756: 1, L0777: 1, L0599: 1, L0608: 1, L0366: 1, S0011: 1, H0653: 1, S0192: 1, S0194: 1, H0543: 1 and S0452: 1.		
61	HQQH90	1212646	71	3 - 680	684	Arg-14 to Cys-25, Ala-90 to Arg-96, Ile-115 to Asp-122, Lys-147 to Ser-152, Ala-202 to Gln-208, Asp-211 to Ser-221.		AR089: 4, AR061: 2 H0457: 11, H0052: 3, H0580: 2, H0529: 2, L0655: 2, L0748: 2, L0439: 2, L0779: 2, H0261: 1, H0486: 1, L0021: 1, H0575: 1, T0071: 1, H0194: 1, L0579: 1, H0087: 1, H0264: 1, T0041: 1, H0695: 1, L0766: 1, L0803: 1, L0775: 1, L0758: 1 and H0422: 1.		
		907532	493	1 - 666	1106	Arg-10 to Cys-21.				
62	HFKHA18	1152242	72	1 - 690	685	Gly-7 to Pro-13, Cys-19 to Gly-25, Phe-51 to Lys-61, Ala-88 to Phe-93, Leu-130 to Ser-136, Ala-221 to Cys-228.		AR089: 4, AR061: 4 H0666: 12, S0358: 10, H0620: 10, L0750: 8, L0747: 7, L0731: 7, H0135: 5, L0659: 5, L0740: 5, L0757: 5,		

[illegible]

63	HFKMA10	964258	73	2 - 766	686	1107	972414	494	1 - 684	1107	Gly-5 to Pro-11, Cys-17 to Gly-23, Phe-49 to Lys-59, Ala-86 to Phe-91, Leu-128 to Ser-134, Asn-209 to Asn-214.	L0776: 1, L0656: 1, L0783: 1, L0383: 1, L0543: 1, L0789: 1, L0663: 1, H0593: 1, H0684: 1, H0659: 1, H0658: 1, H0660: 1, H0709: 1, S0152: 1, H0521: 1, H0627: 1, L0611: 1, L0439: 1, L0745: 1, L0759: 1, L0593: 1, L0361: 1, L0603: 1, S0026: 1, H0667: 1 and H0506: 1.	17q25	114290, 138033, 162100, 170500, 170500, 170500, 180860,
63	HFKMA10	964258	73	2 - 766	686	1107	972414	494	1 - 684	1107	Gly-5 to Pro-11, Cys-17 to Gly-23, Phe-49 to Lys-59, Ala-86 to Phe-91, Leu-128 to Ser-134, Asn-209 to Asn-214.	L0776: 1, L0656: 1, L0783: 1, L0383: 1, L0543: 1, L0789: 1, L0663: 1, H0593: 1, H0684: 1, H0659: 1, H0658: 1, H0660: 1, H0709: 1, S0152: 1, H0521: 1, H0627: 1, L0611: 1, L0439: 1, L0745: 1, L0759: 1, L0593: 1, L0361: 1, L0603: 1, S0026: 1, H0667: 1 and H0506: 1.	17q25	114290, 138033, 162100, 170500, 170500, 170500, 180860,

[illegible]

64	HHBFM91	1092116	74	3 - 506	687	Ala-19 to Phe-24, Thr-45 to Val-53, Ile-77 to Arg-83, Ser-105 to Gly-111, Gln-128 to Ala-144, Asp-153 to Gly-161.	S0031: 1. AR089: 8, AR061: 1 H0575: 2, S0031: 2, S0134: 1, H0156: 1, H0373: 1, H0328: 1, H0135: 1, S0428: 1, H0682: 1, H0435: 1, H0518: 1, H0521: 1, L0779: 1 and L0758: 1.		264470
		912832	495	2 - 343	1108				
65	HIBBF63	912715	75	3 - 419	688	Thr-3 to Arg-10, Lys-71 to Lys-80, Glu-107 to Arg-120, Lys-128 to Gly-133.	L0748: 2, H0052: 1, H0194: 1, T0010: 1, H0658: 1, S0380: 1 and L0366: 1.	16p13.3	141750, 141800, 141800, 141800, 141800, 141850, 141850, 141850, 141850, 141850, 156850, 186580, 191092, 600140, 600273, 601313,

66	HMCEI38	1134410	76	190 - 627	689	Gln-21 to Ala-28, Tyr-55 to Phe-60, Tyr-78 to Ile-84.	AR061: 4, AR089: 2 H0645: 1, H0494: 1, S0142: 1, H0593: 1 and H0435: 1.		601785
		912580	496	189 - 626	1109	Gln-21 to Ala-28, Tyr-55 to Phe-60, Tyr-78 to Ile-84.			
		1154790	77	1181 - 3	690	Pro-7 to Ile-20, Arg-26 to Trp-36, Trp-68 to Thr-88, Pro-96 to Gly-101, Ser-109 to Arg-117, Pro-163 to Ala-169, Asp-260 to Asp-266.	AR061: 6, AR089: 5 H0641: 4, H0521: 4, S0418: 2, H0617: 2, L0794: 2, H0436: 2, L0748: 2, L0596: 2, H0556: 1, S0134: 1, H0650: 1, H0657: 1, H0341: 1, S0001: 1, H0638: 1, S0358: 1, S0045: 1, S0278: 1, S0474: 1, H0545: 1, H0081: 1, H0271: 1, H0416: 1, H0551: 1, H0623: 1, H0059: 1, S0344: 1, L0761: 1, L0803: 1, L0804: 1, L0383: 1, H0435: 1, S0152: 1, H0522: 1,		
67	HMWJD68								

68	HOEOL58	912628	497	14 - 685	1110	Pro-2 to Cys-9, Gly-27 to Glu-32, Thr-87 to Asn-103, Thr-146 to Lys-157, Lys-189 to Val-194, Lys-210 to Arg-218.	L0749: 1, L0753: 1, H0445: 1, H0595: 1 and H0677: 1.		
		1078090	78	66 - 338	691	Glu-11 to Asp-26, Val-71 to Lys-87.			
69	HRACA51	912836	498	3 - 407	1111		AR089: 6, AR061: 5 S0126: 2, H0543: 2, H0539: 1 and S0152: 1.		
		1162856	79	3 - 677	692	Asn-43 to Asn-50, Ala-77 to Gly-92, Thr-103 to Asn-109, Gly-132 to Glu-142, Ile-185 to Gly-196, Arg-207 to Ser-214.			

							H0015: 1, H0107: 1, H0083: 1, H0510: 1, S6028: 1, H0252: 1, H0622: 1, H0272: 1, H0100: 1, H0494: 1, S0144: 1, L0800: 1, L0768: 1, L0794: 1, L0804: 1, L0806: 1, H0689: 1, H0672: 1, S0328: 1, H0631: 1, S0028: 1, L0749: 1, L0750: 1, L0780: 1, L0755: 1, L0759: 1, S0434: 1, L0592: 1, H0668: 1 and H0423: 1.		
70	HSHAV32	1180388	80	157 - 627	693	Asn-40 to Asn-47, Ala-74 to Gly-89, Thr-100 to Asn-106, Gly-129 to Glu-139, Ile-182 to Gly-193, Arg-204 to Ser-211. Phe-49 to Lys-55.		AR089: 4, AR061: 3 L0731: 7, L0749: 6, L0105: 5, H0046: 5, L0748: 5, H0551: 4, L0747: 4, L0777: 4,	

71	HTPDE66	912812	500	117 - 872	1113	Phe-49 to Lys-55.	S0040: 3, L0663: 3, S0152: 3, L0659: 2, H0547: 2, L0439: 2, L0779: 2, L0448: 1, H0685: 1, H0341: 1, H0663: 1, H0580: 1, L0021: 1, H0594: 1, S0214: 1, H0615: 1, H0628: 1, H0561: 1, H0646: 1, L0640: 1, L0662: 1, L0774: 1, L0783: 1, L0809: 1, L0666: 1, H0144: 1, L0352: 1, S3012: 1, S0037: 1, L0754: 1, L0756: 1, L0752: 1, L0755: 1, L0759: 1, H0667: 1 and S0192: 1.		
		912812	500	117 - 872	1113	Phe-49 to Lys-55.	AR061: 6, AR089: 4 L0777: 8, L0744: 7, H0039: 6, L0754: 6, H0046: 4, L0751: 4, H0617: 3, L0372: 3, L0743: 3, L0747: 3, L0750: 3, S0356: 2,		

					S0132: 2, H0549: 2, H0587: 2, L0764: 2, L0773: 2, L0659: 2, L0382: 2, L0809: 2, L0519: 2, H0593: 2, L0752: 2, L0596: 2, L0595: 2, H0506: 2, H0294: 1, H0483: 1, H0661: 1, S0358: 1, S0444: 1, L0717: 1, H0370: 1, H0318: 1, H0234: 1, H0597: 1, H0024: 1, H0622: 1, H0553: 1, H0212: 1, H0135: 1, H0087: 1, H0059: 1, H0100: 1, H0538: 1, L0763: 1, L0772: 1, L0646: 1, L0645: 1, L0648: 1, L0364: 1, L0649: 1, L0774: 1, L0806: 1, L0776: 1, L0657: 1, L0540: 1, L0542: 1, L0383: 1, L0529: 1, L0664: 1, L0665: 1, H0682: 1, H0683: 1,		
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								L0809: 2, H0547: 2, L0754: 2, L0758: 2, L0485: 2, H0484: 1, S0360: 1, H0550: 1, H0441: 1, H0392: 1, H0031: 1, H0644: 1, L0369: 1, L0662: 1, L0768: 1, L0790: 1, L0663: 1, L0664: 1, S0126: 1, H0555: 1, L0756: 1, L0589: 1, L0592: 1, L0599: 1 and H0506: 1.		
75	HUVFX92	912929	503	3 - 320	1116	Ile-12 to Asn-17, Val-74 to His-92.	Asp-47 to Ser-53, Ala-82 to Arg-88.	AR061: 0, AR089: 0 H0623: 2, S0045: 1 and H0620: 1.		
		912672	504	3 - 395	1117	Asp-47 to Ser-53, Ala-82 to Thr-89.				
76	HWAEG71	1182321	86	1 - 717	699	Pro-17 to His-22.		AR089: 6, AR061: 1 L0740: 2 and H0581: 1.		
		931547	505	2 - 553	1118	Gln-60 to Ala-68, Trp-132 to Ser-138, Lys-156 to Val-163.				

77	HWAHD49	1228064	87	151 - 1011	700	3. Arg-12 to Leu-19, Gly-56 to Pro-62, Cys-68 to Gly-74, Phe-100 to Lys-110, Ala-137 to Phe-142, Leu-179 to Ser-185, Ala-278 to Cys-285.	AR089: 9, AR061: 3 S0358: 10, L0747: 7, L0750: 7, L0731: 7, H0620: 5, L0659: 5, S0360: 4, S0022: 4, L0666: 4, L0665: 4, L0748: 4, L0740: 4, L0777: 4, L0757: 4, L0588: 4, H0265: 3, S0420: 3, H0046: 3, H0135: 3, H0100: 3, L0650: 3, L0375: 3, L0382: 3, H0651: 3, S0028: 3, L0755: 3, H0352: 3, S0278: 2, H0592: 2, H0333: 2, H0253: 2, H0544: 2, H0123: 2, H0081: 2, H0012: 2, H0252: 2, H0428: 2, L0763: 2, L0770: 2, L0774: 2, L0518: 2, L0809: 2, H0682: 2, S0037: 2, S0027: 2, L0751: 2, L0758: 2, H0170: 1,		
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79	HWLKF25	912581	507	2 - 565	1120	Pro-334 to Glu-344, Gln-382 to Pro-389.	L0646: 1, L0773: 1, L0803: 1, L0375: 1, L0651: 1, L0636: 1, L0664: 1, H0522: 1, L0439: 1, L0779: 1, L0777: 1, L0731: 1 and H0136: 1.		
						Arg-1 to Gln-15, Thr-52 to His-57, Ala-88 to Gln-99, Ser-114 to His-121, Val-129 to Gly-136.			
79	HWLKF25	1089052	89	224 - 886	702	Val-49 to Gln-56, Ala-85 to Leu-93, Pro-96 to Ala-101, Val-110 to Asn-118, Asp-131 to Glu-136, Lys-146 to Ala-159, Met-164 to Tyr-169, Thr-174 to Thr-180.	AR061: 3, AR089: 2 S0358: 1, H0052: 1, L0803: 1 and L0759: 1.		
						Val-49 to Gln-56, Ala-85 to Leu-93, Pro-96 to Ala-101, Val-110 to Asn-118, Asp-131 to Glu-136, Lys-146 to Ala-159.			

80	H2CBH45	963811	90	2 - 421	703	Met-164 to Tyr-169, Thr-174 to Thr-180, Ser-213 to Gly-218.	AR061: 3, AR089: 3 H0437: 1, S0280: 1, T0110: 1, H0622: 1, L0745: 1, L0746: 1, L0731: 1 and L0596: 1.			
81	HAGDN53	1092161	91	2 - 430	704	Ala-1 to Met-18, Leu-20 to Asn-26, Val-38 to Leu-46, Pro-48 to Gly-53, Leu-81 to Gly-86, Gln-94 to Tyr-99, Glu-101 to Gly-109.	AR050: 17, AR051: 11, AR054: 2, AR089: 1, AR061: 0 S0010: 1 and S0027: 1.			
82	HAMFM39	971347	92	1121 - 2929	705	Pro-9 to Gln-16, Phe-31 to Tyr-40, Gln-61 to Trp-66, Arg-71 to Gln-78, Gly-86 to Arg-92. Gln-1 to Ala-7, Thr-36 to Trp-42, Gly-45 to Gly-52, Glu-77 to Pro-89, Gly-105 to Gly-132, Ser-135 to Glu-162.	AR050: 193, AR054: 122, AR051: 84, AR089: 0, AR061: 0 H0255: 59, H0254: 10, H0617: 9, L0747: 8, S0358: 7, H0486: 6, L0655: 6, H0208: 4.			

						H0545: 4, H0024: 4, S0354: 3, H0250: 3, H0123: 3, H0031: 3, L0659: 3, S0328: 3, L0731: 3, H0583: 2, L0808: 2, L0785: 2, H0662: 2, H0586: 2, H0618: 2, H0253: 2, H0424: 2, H0264: 2, H0488: 2, H0100: 2, L0771: 2, L0806: 2, L0809: 2, H0144: 2, H0689: 2, L0749: 2, L0750: 2, L0779: 2, L0777: 2, H0707: 2, L0595: 2, H0624: 1, H0341: 1, S0356: 1, S0360: 1, H0619: 1, H0411: 1, H0370: 1, H0485: 1, H0635: 1, H0025: 1, H0108: 1, H0318: 1, H0581: 1, T0110: 1, H0231: 1, L0738: 1, H0086: 1, H0271: 1, T0006: 1, H0644: 1, H0181: 1,					
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								H0124: 1, H0087: 1, T0067: 1, H0560: 1, H0646: 1, L0371: 1, L0800: 1, L0764: 1, L0768: 1, L0803: 1, L0774: 1, L0657: 1, L0368: 1, L0787: 1, L0666: 1, L0663: 1, L0665: 1, H0519: 1, H0414: 1, S0378: 1, S0380: 1, H0696: 1, S0044: 1, S0432: 1, L0439: 1, L0780: 1, L0755: 1, H0445: 1 and L0596: 1.		
83	HBGQT03	908173	93	3 - 791	706	Lys-1 to Ala-15, Glu-22 to Val-31, Glu-37 to Thr-48, Leu-143 to Asp-160, Thr-170 to Ala-201, Ala-214 to Asp-219.	AR061: 6, AR089: 3 H0617: 10, L0665: 4, H0333: 3, S0366: 3, L0759: 3, H0599: 2, L0648: 2, L0653: 2, L0664: 2, H0519: 2, H0686: 1, H0484: 1, H0664: 1, H0392: 1, L0622: 1, S0280: 1, H0545: 1, T0010: 1, H0424: 1, H0031: 1,			

84	HBGSJ13							H0181: 1, H0708: 1, H0494: 1, H0633: 1, L0371: 1, L0764: 1, L0773: 1, L0768: 1, L0375: 1, L0651: 1, L0659: 1, L0783: 1, L0789: 1, L0438: 1, H0684: 1, H0670: 1, L0744: 1, L0780: 1, L0755: 1 and L0595: 1.		
		1150790	94	822 - 1	707			AR089: 1, AR061: 0 H0617: 2, H0013: 1, H0271: 1, L0455: 1 and H0539: 1.		
		878322	510	1 - 684	1123					
85	HBIBQ89							AR089: 1, AR061: 0 L0438: 6, L0751: 6, L0439: 5, L0770: 4, H0052: 2, H0620: 2, H0521: 2, L0756: 2, L0731: 2, L0758: 2, L0588: 2, H0556: 1, S0282: 1, H0662: 1, H0402: 1, S0418: 1, T0008: 1, S0222: 1, H0392: 1, H0333: 1,		
		909782	95	2 - 577	708					

									L0021: 1, H0581: 1, S0049: 1, L0471: 1, H0266: 1, L0351: 1, L0772: 1, L0766: 1, L0776: 1, L0659: 1, L0792: 1, H0522: 1, S0027: 1, L0779: 1 and S0011: 1.			
86	HCECM90	945088	96	2 - 577	709	Gly-12 to Gly-31, Asn-38 to Gly-62, Asp-70 to Phe-84, Val-94 to Ser-101, Ala-112 to Ser-125, Lys-140 to Asn-145, Asn-175 to Tyr-180, Arg-187 to Thr-192.		AR061: 2, AR089: 1 H0013: 3, L0439: 2, H0624: 1, H0171: 1, S0040: 1, S0420: 1, H0619: 1, H0156: 1, H0575: 1, H0590: 1, H0052: 1, H0011: 1, H0266: 1, H0494: 1, L0519: 1, H0519: 1, H0555: 1, L0777: 1, L0758: 1, S0436: 1 and H0506: 1.				
87	HCEPH71	522739	97	3 - 410	710	Val-1 to Lys-8, Pro-36 to Lys-41, Gln-49 to Lys-57, Ser-63 to Ser-70, Asp-79 to Gln-92, Asn-103 to Thr-122.		AR089: 1, AR061: 1 H0052: 1 and T0067: 1.				

88	HCFMT57	1175204	98	3 - 1220	711	Arg-4 to Val-12, Glu-19 to Arg-29, Glu-34 to Arg-76.	AR061: 0, AR089: 0 L0157: 2, H0620: 2, L0666: 2, S0001: 1, L0717: 1, H0549: 1, S0222: 1, H0581: 1, H0194: 1, H0015: 1, H0399: 1, H0271: 1, H0688: 1, H0428: 1, H0124: 1, L0637: 1, H0672: 1, L0439: 1, L0750: 1 and H0423: 1.		
		765375	511	380 - 3	1124	Glu-5 to Arg-15, Glu-20 to Arg-62.			
89	HCOMM05	1173146	99	3 - 851	712	Gln-22 to Asp-41, Pro-49 to Thr-58, Leu-99 to Gly-107, Ala-117 to Ala-122, Gln-128 to Trp-134, Pro-136 to Pro-144, Phe-147 to Glu-153, Glu-183 to Val-188, Glu-195 to Glu-200, Glu-257 to Leu-265, Met-275 to Ser-283.	AR089: 1, AR061: 1 H0670: 1		
		925952	512	1 - 840	1125	Gln-19 to Asp-38, Pro-46 to Thr-55,			

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						L0596: 1, L0601: 1, H0542: 1 and H0543: 1.		
93	HDPDA47	929193	103	103 - 906	716	Asp-17 to Leu-34, Asp-44 to Ser-51, Asp-63 to Gly-72, Pro-74 to Gly-83, Thr-97 to Met-102.	AR089: 11, AR061: 3 H0521: 7, H0581: 3, H0422: 3, H0650: 2, H0486: 2, S0002: 2, L0770: 2, L0769: 2, L0766: 2, L0518: 2, L0783: 2, L0777: 2, L0731: 2, H0445: 2, H0556: 1, H0583: 1, H0657: 1, H0656: 1, H0341: 1, H0575: 1, H0457: 1, H0179: 1, H0271: 1, L0055: 1, H0264: 1, H0488: 1, S0426: 1, L0662: 1, L0775: 1, L0655: 1, L0665: 1, S0053: 1, H0702: 1, H0701: 1, H0659: 1, L0754: 1,	

									L0779: 1, L0759: 1 and H0543: 1.					
94	HDPFF24	909232	104	104 - 460	717				AR089: 4, AR061: 1 H0171: 5, S0026: 3, S0400: 2, L0471: 2, H0031: 2, H0553: 2, H0547: 2, H0521: 2, L0759: 2, H0423: 2, H0170: 1, H0583: 1, H0656: 1, S0001: 1, S0358: 1, S0360: 1, H0244: 1, H0349: 1, H0590: 1, H0310: 1, H0014: 1, H0039: 1, S0366: 1, H0551: 1, L0351: 1, H0509: 1, S0150: 1, L0369: 1, L0796: 1, L0773: 1, L0662: 1, L0766: 1, L0803: 1, L0635: 1, L0540: 1, H0519: 1, H0684: 1, H0660: 1, H0666: 1, S0044: 1, H0478: 1, H0479: 1, H0626: 1, L0748: 1, L0740: 1, L0777: 1,					

[illegible]

95	HDPPO35	966248	105	72 - 1202	718	Lys-7 to Gly-69, Lys-82 to Lys-88, Ser-94 to Asp-112, Ala-126 to Asp-131, Tyr-134 to Ser-140, Ser-147 to Phe-156, Asp-159 to Ser-165, Thr-176 to Asp-186, Glu-230 to Leu-250, Glu-291 to Arg-298, Gln-313 to Glu-320, Asn-331 to Gly-343, Ser-348 to Leu-363.	Lys-7 to Gly-69, Lys-82 to Lys-88, Ser-94 to Asp-112, Ala-126 to Asp-131, Tyr-134 to Ser-140, Ser-147 to Phe-156, Asp-159 to Ser-165, Thr-176 to Asp-186, Glu-230 to Leu-250, Glu-291 to Arg-298, Gln-313 to Glu-320, Asn-331 to Gly-343, Ser-348 to Leu-363.	L0752: 1, L0755: 1 and H0543: 1.	AR089: 1, AR061: 0 H0521: 15, H0638: 5, H0580: 5, H0271: 5, H0641: 5, H0560: 4, H0090: 3, H0591: 3, L0766: 3, H0542: 3, H0543: 3, H0586: 2, H0497: 2, H0581: 2, L0655: 2, H0518: 2, H0522: 2, L0754: 2, L0747: 2, H0657: 1, H0393: 1, H0431: 1, H0250: 1, H0635: 1, L0021: 1, H0014: 1, H0179: 1, H0416: 1, H0488: 1, L0475: 1, H0359: 1, H0625: 1, S0426: 1, L0598: 1, L0667: 1, L0803: 1, L0804: 1, L0775: 1, L0651: 1, L0659: 1, L0792: 1, L0663: 1, S0428: 1, H0672: 1, H0555: 1, H0436: 1,		
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96	HDPSR74	911396	106	212 - 583	719	Leu-31 to Ser-39, Val-57 to Trp-63, Pro-103 to Gln-111, Leu-118 to Leu-124.	AR050: 48, AR054: 42, AR051: 35, AR089: 3, AR061: 1 H0575: 2, H0580: 1, S0002: 1, S0426: 1, H0521: 1, H0436: 1 and L0748: 1.			
97	HDTKQ14	886936	107	1 - 555	720	Ser-60 to Thr-71, Thr-82 to Leu-94, Gln-113 to Asp-123, Val-125 to Tyr-133, Leu-144 to Gly-149.	AR054: 60, AR051: 40, AR050: 36, AR089: 5, AR061: 2 H0521: 4, H0486: 2, S0002: 2, L0770: 2, L0769: 2, L0766: 2, L0518: 2, L0783: 2, L0777: 2, L0731: 2, H0422: 2, H0556: 1, H0583: 1, H0650: 1, H0657: 1, H0179: 1, L0055: 1, H0488: 1, S0426: 1, L0662: 1, L0775: 1, L0655: 1, L0665: 1, S0053: 1, H0659: 1, L0754: 1, L0779: 1, L0759: 1 and			

98	HE6GF02	1150897	108	804 - 1	721	Gln-13 to Ser-18, Glu-32 to Gly-37, Ala-44 to Trp-49, Glu-56 to Val-61, Gln-68 to Lys-74, Ala-83 to Glu-88, Arg-111 to Gly-117, Tyr-123 to His-143, Ser-167 to Thr-202.	H0543: 1. AR061: 7, AR089: 4 H0100: 1 and H0521: 1.		
		911263	514	1 - 264	1127	Gln-13 to Ser-18, Glu-32 to Gly-37, Ala-44 to Trp-49.			
99	HE8PK12	909884	109	2 - 367	722	Val-30 to Ser-37, Gln-43 to Asp-62, Pro-74 to Glu-79, Thr-102 to Phe-109.	AR089: 6, AR061: 4 L0754: 6, L0777: 6, L0740: 5, L0731: 4, L0758: 4, L0759: 4, S0001: 3, S0280: 3, L0770: 3, L0764: 3, L0747: 3, L0749: 3, L0366: 3, S0412: 3, S0007: 2, H0411: 2, H0013: 2, L0471: 2, T0004: 2, L0598: 2, L0638: 2, L0662: 2, L0783: 2, L0438: 2,		

Table 9.20

									H0696: 2, L0744: 2, L0748: 2, L0751: 2, L0745: 2, L0779: 2, L0752: 2, H0170: 1, S0282: 1, H0662: 1, H0574: 1, T0060: 1, H0427: 1, H0590: 1, S0010: 1, L0105: 1, S0049: 1, H0194: 1, H0373: 1, L0163: 1, H0201: 1, H0031: 1, H0553: 1, S0306: 1, L0776: 1, L0659: 1, L0526: 1, L0809: 1, L0663: 1, H0144: 1, H0547: 1, H0648: 1, H0672: 1, L0743: 1, L0780: 1, S0031: 1, H0343: 1, L0604: 1 and H0653: 1.				
100	HE9SE62	911476	110	1 - 564	723				AR061: 16, AR089: 6 L0804: 1, S0052: 1, H0144: 1 and H0659: 1.				
101	HEOPL36	1195682	111	86 - 487	724	Gly-11 to Thr-16, Ser-35 to Ser-56, Thr-58 to Ser-73.			AR089: 18, AR061: 5 L0740: 11, L0439: 9, L0748: 8, H0616: 5.				

									S0434: 2, S0354: 1, N0006: 1, H0622: 1 and H0478: 1.			
103	HFTDF15	657020	113	129 - 254	726				AR089: 3, AR061: 2 H0563: 1 and H0123: 1.			
104	HHEQV39	932851	114	1 - 711	727			Leu-7 to Phe-27, Gln-50 to Gln-57.	AR089: 3, AR061: 1 T0042: 1, H0543: 1 and H0422: 1.			
105	HHFCK09	965304	115	2692 - 389	728			Tyr-47 to Glu-58, Lys-70 to Gly-77, Pro-121 to Leu-126, Leu-150 to Leu-158, Asn-166 to Glu-171, Arg-417 to Ser-425, Phe-465 to Cys-473, Ser-485 to Asn-492, Ser-497 to Ala-504, Gln-531 to Trp-537, Asp-557 to Glu-562.	AR089: 3, AR061: 2 L0666: 8, L0439: 6, H0253: 5, H0046: 4, L0769: 4, H0295: 3, H0255: 3, L0747: 3, L0756: 3, L0779: 3, H0657: 2, H0618: 2, H0318: 2, H0622: 2, H0068: 2, L0667: 2, L0772: 2, L0776: 2, L0663: 2, H0520: 2, H0593: 2, H0670: 2, H0521: 2, L0750: 2, L0759: 2, L0593: 2, L0601: 2, S0116: 1, H0341: 1, S0212: 1, H0306: 1, H0402: 1.			

						L0617: 1, S0358: 1, H0609: 1, H0592: 1, H0333: 1, T0040: 1, H0013: 1, H0635: 1, H0575: 1, H0036: 1, H0581: 1, H0123: 1, H0050: 1, H0012: 1, H0071: 1, T0010: 1, H0687: 1, H0290: 1, H0617: 1, H0606: 1, H0038: 1, H0487: 1, H0494: 1, H0334: 1, S0150: 1, H0647: 1, S0142: 1, L0640: 1, L0639: 1, L0637: 1, L0641: 1, L0768: 1, L0649: 1, L0514: 1, L0659: 1, L0783: 1, L0788: 1, L0664: 1, L0665: 1, L0438: 1, H0547: 1, H0435: 1, H0522: 1, H0696: 1, S0404: 1, H0478: 1, L0742: 1, L0740: 1, L0749: 1, L0758: 1, S0434: 1, S0194: 1,		
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108	HLW63	908437	118	404 - 2566	731	Thr-7 to Phe-29, Thr-37 to Lys-52, Glu-89 to Val-112.	AR051: 11, AR050: 9, AR054: 5, AR089: 0, AR061: 0 H0031: 5, S0222: 4, S0028: 4, H0662: 3, L0748: 3, S0260: 3, S0276: 3, S0282: 2, S0360: 2, S0046: 2, H0575: 2, H0196: 2, S0036: 2, H0268: 2, L0662: 2, S0027: 2, L0754: 2, L0747: 2, L0749: 2, L0756: 2, L0777: 2, L0604: 2, L0595: 2, H0171: 1, S0030: 1, S0029: 1,	H0509: 1, H0529: 1, L0520: 1, L0761: 1, L0650: 1, L0809: 1, L0666: 1, L0665: 1, S0126: 1, H0684: 1, H0648: 1, S0390: 1, L0740: 1, L0745: 1, L0749: 1, L0750: 1, L0755: 1, L0591: 1, L0362: 1 and S0242: 1.		
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111	HMSHO64	746582	121	1 - 411	734	Ser-11 to Ser-21, Ser-84 to Ala-89, Pro-98 to Arg-107.	AR089: 2, AR061: 2 S0002: 2		
112	HMTAW83	911385	122	1 - 363	735	Ile-26 to Trp-33, Glu-52 to Leu-71.	AR089: 0, AR061: 0 H0583: 1, H0644: 1, L0766: 1 and H0518: 1.		
113	HMVAM09	963814	123	2 - 802	736		AR089: 4, AR061: 1 L0731: 7, L0517: 5, S0212: 3, L0775: 3, L0740: 3, H0266: 2, L0809: 2, H0696: 2, L0748: 2, S0132: 1, H0574: 1, H0013: 1, H0544: 1, H0023: 1, H0071: 1, H0286: 1, H0100: 1, H0494: 1, S0370: 1, L0770: 1, L0646: 1, L0764: 1, L0771: 1, L0363: 1, L0774: 1, L0659: 1, L0789: 1, L0666: 1, S0126: 1, H0522: 1, L0754: 1, L0747: 1 and L0755: 1.		
114	HNSAA28	946988	124	85 - 1557	737	Glu-9 to Ser-20, Ile-23 to Gly-29,	AR050: 8, AR054: 6, AR051: 3, AR089: 1,		

							Pro-50 to Cys-66, Pro-74 to Glu-79, Glu-93 to Trp-98, Thr-121 to Ser-133, Leu-180 to Lys-196, Thr-213 to Glu-225, Glu-234 to Glu-240, Arg-263 to Glu-270, Glu-283 to Ala-298, Lys-318 to Ala-336, Val-340 to Ala-351, Val-361 to Pro-372, Asn-445 to Pro-468, Pro-475 to Lys-491.	AR061: 1 H0036: 2, L0766: 2, H0686: 1, H0622: 1, H0625: 1, L0791: 1, L0779: 1 and S0434: 1.					
						972348	516	3 - 452	1129	Thr-1 to Ala-10, Val-20 to Pro-31, Asn-104 to Thr-124.			
115	HOGEQ43	1226207	125	494 - 2083	738					Lys-1 to Thr-34, Phe-80 to Gly-85, Tyr-91 to Ser-105, Thr-122 to Ala-133, Ser-151 to Ala-157, Glu-208 to Trp-213, His-219 to Trp-224, Glu-237 to Glu-244, Asn-251 to Ser-256.	AR089: 1, AR061: 0 H0457: 8, L0766: 7, L0599: 6, H0677: 6, L0438: 5, L0779: 5, H0012: 3, L0809: 3, H0656: 2, H0620: 2, L0771: 2, H0435: 2, H0436: 2, L0748: 2, L0439: 2, L0751: 2		

116	HOUDHI9					Gln-291 to Trp-296, Asn-311 to Phe-321, Ser-327 to Glu-335, Lys-364 to Trp-369, Ala-376 to Gly-384, Asn-437 to Trp-444, Met-462 to Trp-472, Gln-483 to Gly-491, Thr-499 to Trp-504, Arg-512 to Ala-517.	L0749: 2, S0134: 1, H0645: 1, H0587: 1, H0635: 1, H0581: 1, H0546: 1, H0477: 1, H0560: 1, H0641: 1, S0422: 1, H0529: 1, L0521: 1, L0662: 1, L0794: 1, L0774: 1, L0775: 1, L0606: 1, L0659: 1, L0647: 1, L0789: 1, L0791: 1, L0792: 1, L0666: 1, L0663: 1, L0665: 1, H0702: 1, H0547: 1, H0576: 1, S0028: 1, L0756: 1, L0777: 1, L0755: 1, L0758: 1, H0543: 1 and H0506: 1.		
		935465	517	1 - 150	1130	Glu-1 to Thr-13.			
		1150918	126	506 - 3	739	Pro-8 to Ser-13.	AR089: 1, AR061: 0 S0040: 1, H0250: 1, T0048: 1, L0761: 1, L0764: 1, L0783: 1, L0809: 1, L0789: 1 and L0757: 1.		
		908588	518	52 - 573	1131	Thr-8 to Gln-19,			

117	HOUFT36	911293	127	160 - 846	740	Lys-26 to Glu-33, Lys-41 to Ile-50. Lys-27 to Ile-43.	AR089: 2, AR061: 1 L0794: 6, L0598: 2, L0803: 2, L0748: 2, S0040: 1, S0046: 1, H0431: 1, H0318: 1, L0766: 1, L0606: 1, L0749: 1, L0758: 1 and S0192: 1.		
118	HPMFL08	959569	128	191 - 346	741	Met-43 to Trp-52.	AR089: 1, AR061: 1 H0031: 2		
119	HRSMD49	723025	129	190 - 456	742	Gln-36 to Ile-46, Ser-55 to Phe-65, Ser-67 to Lys-78.	AR089: 3, AR061: 2 H0394: 1 and L0589: 1.		
120	HSDII69	917180	130	202 - 540	743	His-13 to Gly-21, Tyr-61 to Asp-66, Ala-105 to Thr-110.	AR061: 6, AR089: 5 H0328: 4, H0031: 3, L0519: 3, L0748: 2, L0777: 2, L0731: 2, S0260: 2, H0624: 1, S6024: 1, H0650: 1, S0116: 1, H0254: 1, S0007: 1, H0393: 1, H0441: 1, H0438: 1, H0574: 1, H0156: 1, H0599: 1, S0051: 1,		

									L0763: 1, L0772: 1, L0764: 1, L0771: 1, L0773: 1, L0650: 1, L0806: 1, L0659: 1, L0547: 1, L0809: 1, L0666: 1, L0663: 1, L0665: 1, S0328: 1, S0380: 1, S0390: 1, S0032: 1, L0744: 1, L0745: 1, L0746: 1, L0747: 1, L0756: 1, L0777: 1, L0758: 1, L0588: 1, S0276: 1, S0196: 1, S0412: 1 and H0506: 1.			
122	HSFAM09	1150965	132	2 - 325	745	Leu-2 to Gly-8.	Arg-1 to Ser-8, Lys-42 to Lys-48.	AR061: 5, AR089: 2 H0154: 2				
		573345	519	147 - 332	1132							
123	HSSAX53	507509	133	209 - 361	746			H0135: 1 and H0063: 1.				
124	HSVAW49	1150960	134	220 - 486	747	Pro-19 to Thr-24, Thr-78 to Lys-89.	Glu-21 to Glu-27.	AR061: 9, AR089: 7 H0309: 1				
		689674	520	44 - 208	1133							
125	HTEAG49	954614	135	510 - 208	748			AR089: 1, AR061: 0 L0759: 4, L0770: 2,				

									S0040: 1, S0318: 1, S0334: 1, S0316: 1, S0340: 1, H0038: 1, L0598: 1, L0800: 1 and S0276: 1.		
126	HTLBH67	751985	136	1 - 282	749				AR061: 2, AR089: 1 L0752: 3, L0747: 2, H0294: 1, H0253: 1, H0046: 1, H0040: 1, H0063: 1, H0494: 1, S0352: 1, L0769: 1, L0766: 1, L0804: 1, L0805: 1, L0791: 1, H0521: 1, L0779: 1, L0780: 1, L0731: 1 and L0758: 1.		
127	HTLJC71	922923	137	3 - 1355	750			His-1 to Phe-9, Cys-13 to Thr-18, Pro-35 to Gly-48, Glu-61 to Pro-68, Lys-105 to Ala-136, Thr-144 to Gln-154, Leu-163 to Gly-171, Thr-205 to Gln-222, Pro-251 to Gln-257.	AR061: 7, AR089: 5 H0618: 12, H0253: 8, H0038: 6, L0758: 6, L0779: 5, H0616: 3, T0041: 1, L0776: 1, S0274: 1 and H0543: 1.		
128	HTPAD46	503313	138	103 - 309	751			His-50 to Leu-69.	AR061: 0, AR089: 0		

									L0794: 4, H0039: 2, S0358: 1, H0013: 1, H0575: 1, L0770: 1, L0769: 1 and L0749: 1.		
129	HTTKP07	911390	139	2 - 337	752	Thr-15 to Asp-25, Glu-69 to Leu-89.			AR089: 1, AR061: 1 H0634: 2		
130	HUCOW17	933357	140	155 - 856	753	Gln-27 to Trp-45.			AR089: 4, AR061: 2 L0439: 5, S0002: 3, L0604: 3, H0619: 2, H0024: 2, H0625: 2, L0768: 2, L0757: 2, H0638: 1, S0420: 1, S0360: 1, H0586: 1, L0163: 1, S0214: 1, L0143: 1, H0264: 1, L0769: 1, L0764: 1, L0774: 1, L0651: 1, L0659: 1, L0542: 1, L0789: 1, H0539: 1, H0521: 1, S0044: 1, L0777: 1, L0758: 1, L0599: 1 and H0422: 1.		
131	HWHGF52	726102	141	1 - 453	754	Gln-1 to Lys-8, Gly-10 to Trp-17, Val-28 to Gly-43, Thr-54 to Glu-63.			AR089: 1, AR061: 0 L0776: 5, L0764: 4, L0743: 4, L0740: 3, L0750: 3, L0777: 3,		

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132	HWHHB69	1212612	142	2 - 2176	755	Glv-1 to Ser-7,	AR089: 1, AR061: 1	L0731: 3, S0001: 2, H0438: 2, H0052: 2, H0194: 2, H0201: 2, L0526: 2, H0144: 2, L0742: 2, H0662: 1, H0619: 1, H0261: 1, H0392: 1, H0455: 1, H0586: 1, H0587: 1, H0574: 1, H0486: 1, H0013: 1, H0427: 1, S0010: 1, S0346: 1, T0110: 1, H0009: 1, L0157: 1, H0320: 1, H0051: 1, T0006: 1, H0604: 1, H0163: 1, H0646: 1, L0763: 1, L0638: 1, L0630: 1, L0646: 1, L0773: 1, L0651: 1, L0523: 1, L0805: 1, L0666: 1, L0663: 1, L0664: 1, H0547: 1, H0660: 1, S0404: 1, L0744: 1, L0439: 1, L0752: 1, S0434: 1 and L0595: 1.		
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					Ala-70 to Tyr-77, Arg-130 to Ser-140.	L0803: 3, S0354: 2, H0052: 2, H0617: 2, L0770: 2, L0646: 2, S0028: 2, L0753: 2, H0445: 2, H0556: 1, S6024: 1, H0657: 1, S0418: 1, S0420: 1, H0351: 1, H0441: 1, H0586: 1, H0013: 1, S0280: 1, H0156: 1, L0021: 1, H0122: 1, S0010: 1, H0571: 1, L0163: 1, H0135: 1, H0412: 1, H0100: 1, L0351: 1, L0769: 1, L0639: 1, L0764: 1, L0649: 1, L0659: 1, L0809: 1, L0530: 1, H0520: 1, H0547: 1, H0519: 1, H0690: 1, H0539: 1, S0136: 1, H0696: 1, L0748: 1, L0747: 1, L0756: 1, L0779: 1, L0757: 1, S0434: 1, S0436: 1, S0011: 1 and H0136: 1.	
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		690442	521	1 - 261	1134	Gly-1 to Ser-7.			
133	HWLFH94	1151387	143	695 - 333	756		AR089: 5, AR061: 2 S0358: 5, L0596: 3, L0771: 2, L0758: 2, S0354: 1, S0376: 1, T0109: 1, H0036: 1, H0590: 1, L0040: 1, H0038: 1, H0616: 1, L0646: 1, L0764: 1, L0768: 1, L0775: 1, L0659: 1 and S0404: 1.		
		909682	522	134 - 535	1135	Ser-25 to Ala-52, Phe-64 to Glu-71.			
134	HWMBM13	909683	144	3 - 539	757	Pro-11 to Ala-35, Phe-47 to Glu-54, Glu-78 to Gly-83, Gln-94 to Ser-106, Ser-114 to Val-120.	AR089: 2, AR061: 2 S0358: 6, L0794: 4, L0758: 4, S0354: 3, L0779: 3, L0596: 3, S0376: 2, H0036: 2, H0620: 2, H0063: 2, L0771: 2, L0803: 2, L0654: 2, L0659: 2, T0109: 1, H0013: 1, H0590: 1, H0052: 1, H0596: 1, T0110: 1, L0040: 1, H0090: 1, H0038: 1, H0040: 1,		

135	HWWDN34	911357	145	2 - 1000	758	Ser-11 to Leu-17, Pro-20 to Val-26, Ser-87 to Lys-95, Thr-109 to Lys-116, Pro-164 to Gln-170, Glu-222 to Ser-227, Ser-292 to Gln-303, Asp-315 to Gly-324, Gly-326 to Ala-333.	H0616: 1, H0429: 1, H0561: 1, L0646: 1, L0764: 1, L0768: 1, L0766: 1, L0775: 1, L0790: 1, L0792: 1, S0404: 1, S0390: 1, L0777: 1, L0755: 1, L0592: 1 and S0458: 1.		
136	HCEML27	997051	146	750 - 61	759	Pro-93 to Asp-102, Pro-112 to Ala-119, Ser-131 to Pro-150, Glu-188 to Gly-196.	AR089: 1, AR061: 1 S0354: 16, H0457: 7, L0758: 3, H0555: 2, H0170: 1, H0657: 1, H0255: 1, H0662: 1, S0360: 1, H0036: 1, H0150: 1, H0051: 1, H0553: 1, L0800: 1, L0644: 1, L0771: 1, L0803: 1, L0787: 1, L0663: 1, H0144: 1, S0374: 1, H0670: 1, H0522: 1, L0749: 1, S0452: 1 and H0506: 1.		

		952634	525	2 - 1567	1138	Thr-2 to Asp-9, Val-31 to Pro-55, Gly-66 to Glu-72, Pro-74 to Pro-79, Phe-91 to Val-118, Pro-129 to Pro-144.				
139	HSBBF79	965764	149	3 - 707	762	Gln-2 to Glu-12.	AR061: 520, AR089: 428 S0040: 1, H0669: 1, H0662: 1, S0420: 1, S0358: 1, S0376: 1, H0632: 1, T0040: 1, T0110: 1, H0633: 1, L0800: 1, H0666: 1, S0152: 1, S0028: 1, L0581: 1 and L0594: 1.			
140	HSLKA77	1204269	150	22 - 1137	763		AR061: 4, AR089: 3 L0748: 20, L0731: 8, L0755: 6, H0031: 5, H0644: 5, H0090: 5, L0775: 5, L0749: 5, S0360: 4, L0770: 4, L0766: 4, L0740: 4, L0754: 4, L0777: 4, L0757: 4, L0758: 4, H0050: 3, L0764: 3,			

						L0768: 3, L0666: 3, L0665: 3, L0750: 3, L0756: 3, S0212: 2, H0580: 2, H0545: 2, H0123: 2, L0471: 2, H0012: 2, S0022: 2, H0622: 2, H0553: 2, H0383: 2, S0344: 2, L0662: 2, L0657: 2, L0663: 2, L0664: 2, H0144: 2, H0555: 2, S0390: 2, L0743: 2, L0747: 2, L0759: 2, L0581: 2, L0599: 2, H0265: 1, H0295: 1, T0049: 1, S0358: 1, H0619: 1, L0717: 1, H0592: 1, H0486: 1, L0477: 1, T0039: 1, T0040: 1, H0013: 1, S0010: 1, H0318: 1, H0052: 1, H0046: 1, H0023: 1, H0051: 1, T0079: 1, H0355: 1, H0510: 1, H0290: 1, S0250: 1, H0628: 1,
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141	hagdr21	911589	526	88 - 414	1139	Pro-52 to Asp-57, Asp-67 to Trp-72, Lys-87 to Gly-92, Asp-98 to Gly-104.	L0456: 1, H0316: 1, H0040: 1, H0264: 1, H0623: 1, H0494: 1, S0016: 1, S0210: 1, L0761: 1, L0771: 1, L0650: 1, L0774: 1, L0375: 1, L0784: 1, L0776: 1, L0655: 1, H0547: 1, H0659: 1, H0670: 1, H0672: 1, H0696: 1, S0037: 1, S0028: 1, S0032: 1, L0744: 1, L0779: 1, L0752: 1, L0753: 1, S0031: 1 and L0366: 1.		
		1090433	151	74 - 1183	764	Gly-36 to Asp-42, Pro-51 to Ala-56, Gln-84 to Leu-91, His-105 to His-112, Tyr-115 to Pro-124, Pro-155 to Ser-162, Cys-167 to Ala-173,	AR061: 3, AR089: 1 S0222: 1, S6014: 1, S0010: 1, S6028: 1 and S0036: 1.		

142	HHFNFH27	1025277	152	252 - 1634	765	His-178 to Leu-190, Ser-217 to Ala-224, Pro-226 to Gly-234, Lys-270 to Ala-275, Pro-316 to Lys-323. Gly-10 to Asp-16, Pro-25 to Ala-30, Gln-58 to Leu-65. Arg-13 to Gly-21, Arg-24 to Gly-31, Ser-41 to Gln-73, Glu-83 to Gly-92, Asp-98 to Ala-103, Asn-105 to Gln-115, Glu-129 to Glu-135, Asp-142 to Gly-147, Val-149 to Met-154, His-171 to Lys-177, Pro-187 to Gly-196, Ala-199 to Cys-208, Arg-230 to Tyr-245, Glu-249 to His-256, Asn-265 to Phe-270, Val-277 to Arg-286, Ala-292 to Asp-300, Leu-327 to Pro-351.	AR089: 81, AR061: 32 H0341: 9, H0657: 7, S0358: 4, H0251: 4, H0428: 4, L0748: 4, L0750: 4, H0445: 4, S0116: 3, H0333: 3, H0318: 3, T0041: 3, S0126: 3, H0670: 3, H0648: 3, H0543: 3, H0170: 2, S0376: 2, S0360: 2, S0007: 2, H0619: 2, H0393: 2, H0486: 2, H0156: 2, H0596: 2, H0046: 2, H0014: 2, H0059: 2, T0004: 2, H0647: 2, L0521: 2, L0375: 2, L0517: 2, H0659: 2.		
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143	HTLIT05	1217625	153	81 - 623	766			L0599: 1, L0608: 1, L0594: 1, L0603: 1, H0668: 1, H0665: 1, H0667: 1, S0194: 1, H0542: 1, H0423: 1, H0422: 1, S0424: 1 and H0506: 1.		
144	HAPNV33	1151374	154	1 - 774	767			AR061: 7, AR089: 2 H0619: 1, H0575: 1, H0615: 1 and S0028: 1.		
145	HBTAE84	1128800	155	3 - 416	768			AR089: 1, AR061: 0 S0180: 1		
146	HDPVY89	827026	156	2 - 580	769			AR089: 4, AR061: 3 H0657: 3, H0253: 3,		

						Arg-133 to Leu-141, Gly-182 to Asp-187.	H0494: 3, H0521: 3, L0593: 3, H0437: 2, H0587: 2, H0559: 2, H0620: 2, H0428: 2, L0769: 2, L0666: 2, H0547: 2, S0028: 2, L0439: 2, H0556: 1, H0662: 1, H0125: 1, S0418: 1, H0619: 1, L0021: 1, H0618: 1, H0318: 1, H0052: 1, H0545: 1, H0009: 1, H0172: 1, H0012: 1, H0266: 1, H0181: 1, H0617: 1, H0673: 1, S0364: 1, H0135: 1, H0087: 1, H0059: 1, H0529: 1, L0763: 1, L0662: 1, L0766: 1, L0803: 1, L0791: 1, L0438: 1, H0519: 1, H0682: 1, H0539: 1, H0134: 1, H0436: 1, H0576: 1, S0037: 1, S0206: 1, S0032: 1, L0601: 1, H0665: 1,				
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147	HGLDB21	1010920	157	240 - 1388	770	Leu-20 to Pro-34, Lys-36 to Leu-55, Arg-63 to Gln-72, Pro-215 to Thr-222, Ile-288 to Leu-297, Ala-337 to Gly-346.	S0424: 1, H0506: 1 and H0008: 1. AR061: 10, AR089: 4 H0688: 2, L0803: 2, L0666: 2, L0749: 2, L0777: 2, L0594: 2, S0218: 1, H0657: 1, H0656: 1, H0341: 1, H0663: 1, H0351: 1, H0370: 1, H0318: 1, T0103: 1, H0024: 1, H0652: 1, L0769: 1, L0800: 1, L0794: 1, L0766: 1, L0561: 1, L0804: 1, L0657: 1, L0636: 1, L0635: 1, L0789: 1, L0663: 1, L0665: 1, L0750: 1 and H0216: 1.		
		455474	531	3 - 230	1144	Ala-30 to Gly-39.			
148	HMIAN37	947881	158	1 - 645	771	Asp-60 to Lys-75, Glu-136 to Gln-142.	AR061: 2, AR089: 1 S0414: 26, L0439: 12, L0766: 10, L0779: 10, L0777: 10, L0758: 10, L0757: 8, L0752: 7, L0740: 5, H0170: 4,		

					S0354: 4, L0471: 4, L0794: 4, L0653: 4, L0809: 4, L0666: 4, L0748: 4, H0441: 3, H0051: 3, H0266: 3, S0003: 3, H0644: 3, H0032: 3, L0770: 3, L0803: 3, L0664: 3, H0658: 3, S0380: 3, S3014: 3, S0206: 3, L0754: 3, L0750: 3, L0731: 3, S0192: 3, H0657: 2, S0298: 2, S0358: 2, S0360: 2, L0717: 2, S6016: 2, H0574: 2, T0040: 2, H0013: 2, H0052: 2, H0009: 2, S6028: 2, H0428: 2, H0090: 2, H0591: 2, S0422: 2, L0804: 2, L0659: 2, L0663: 2, L0665: 2, H0144: 2, H0689: 2, H0521: 2, S3012: 2, S0037: 2, S0028: 2, L0742: 2, L0745: 2,				
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								H0529: 1, L0637: 1, L0641: 1, L0764: 1, L0771: 1, L0773: 1, L0662: 1, L0649: 1, L0388: 1, L0774: 1, L0607: 1, L0636: 1, L0783: 1, L0647: 1, L0790: 1, S0374: 1, L0438: 1, H0519: 1, S0126: 1, S0378: 1, H0518: 1, H0696: 1, H0436: 1, S0027: 1, L0744: 1, L0749: 1, L0755: 1, L0759: 1, H0445: 1, L0581: 1, S0011: 1, H0653: 1, S0242: 1, H0422: 1, S0042: 1 and S0424: 1.		
149	HODAK55	1110333	159	361 - 2	772	Cys-52 to Trp-58, His-61 to Phe-68.		AR061: 11, AR089: 9 L0748: 3 and H0328: 1.		
		745532	532	2 - 169	1145					
150	HSLEI59	1128801	160	770 - 267	773			AR089: 1, AR061: 1 S0028: 2, H0171: 1, H0318: 1, S0216: 1, S0044: 1 and S0031: 1		

151	HSQFH29	781945	533	3 - 470	1146	Thr-32 to Phe-42, Leu-49 to Asn-54.	AR089: 14, AR061: 12 S0026: 2, S0045: 1 and L0375: 1.			
		1217061	161	2 - 1723	774	Glu-33 to Arg-47, Glu-75 to Phe-87, Tyr-167 to Lys-173, Pro-199 to Ala-204, Arg-249 to Lys-256, Leu-319 to Asn-324, Pro-385 to Glu-390, Val-441 to Val-448, Asn-512 to Ile-517.				
		967708	534	46 - 462	1147					
152	HTLEA35	1107230	162	503 - 3	775		AR089: 25, AR061: 15 H0545: 3, H0265: 2, H0424: 2, H0556: 1, S0470: 1, H0663: 1, S0420: 1, H0443: 1, H0559: 1, H0253: 1, H0086: 1, H0388: 1 and H0087: 1.			
		827028	535	3 - 371	1148	Ala-4 to Phe-11, Pro-28 to Arg-35, Ala-49 to Lys-57, Asp-62 to Cys-67.				
153	HUVGG63	1204716	163	1 - 1467	776	Phe-4 to Arg-13, Arg-20 to Pro-27,	AR089: 1, AR061: 1 H0556: 14, L0751: 12,			

Thr-29 to Ala-38, Asp-48 to Thr-54, Ala-68 to Glu-78, Ser-101 to Ile-108, Asp-117 to Gln-162, Thr-206 to Trp-212, Cys-285 to Lys-300, Gly-311 to Gly-316, Thr-362 to Thr-367, Arg-376 to Ser-382, Pro-413 to Pro-418, Ser-430 to Gly-435, Asp-484 to Ser-489.	L0777: 11, H0265: 7, L0769: 7, L0747: 5, H0052: 4, L0764: 4, L0438: 4, L0741: 4, L0604: 4, S0358: 3, H0266: 3, H0424: 3, S0344: 3, L0775: 3, L0776: 3, L0758: 3, S0212: 2, H0402: 2, S0007: 2, S0046: 2, S0132: 2, S0222: 2, H0253: 2, S0051: 2, H0594: 2, H0328: 2, H0213: 2, H0617: 2, H0674: 2, H0412: 2, H0100: 2, H0647: 2, S0002: 2, L0761: 2, L0774: 2, L0809: 2, S0152: 2, L0742: 2, L0439: 2, L0755: 2, L0757: 2, H0445: 2, L0594: 2, H0542: 2, H0543: 2, H0484: 1, H0254: 1, H0255: 1, H0125: 1, S0418: 1, S0360: 1, H0580: 1,
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						H0547: 1, S0126: 1, H0690: 1, S0330: 1, H0539: 1, H0576: 1, S0322: 1, S0027: 1, S0206: 1, S0032: 1, L0740: 1, L0754: 1, L0749: 1, L0750: 1, L0779: 1, L0752: 1, H0444: 1, H0707: 1, S0194: 1, H0423: 1 and S0424: 1.		
154	HAGAX57	969432	536	3 - 1448	1149	Tyr-7 to Tyr-15, Pro-43 to Ala-52, Gln-57 to Ala-62, Asn-68 to Ala-73, Tyr-75 to Met-83, Glu-115 to Leu-140, Ala-144 to Glu-156, Val-159 to Ser-166, Arg-178 to Pro-186, Arg-191 to Ile-198.	AR061: 9, AR089: 4 L0748: 13, L0752: 8, L0438: 4, H0212: 3, S0328: 3, S0010: 2, L0764: 2, L0776: 2, L0659: 2, L0749: 2, L0779: 2, L0599: 2, H0170: 1, T0104: 1, H0331: 1, H0574: 1, H0052: 1, H0596: 1, S0050: 1, H0051: 1, L0483: 1, H0032: 1, H0068: 1, S0466: 1, S0422: 1, L0800: 1,	

									L0803: 1, L0651: 1, L0791: 1, H0539: 1, H0521: 1, L0780: 1, L0753: 1, L0758: 1 and S0192: 1.		
155	HAMGX15	949211	537	185 - 778	1150				Tyr-7 to Tyr-15, Pro-43 to Ala-52, Gln-57 to Ala-62, Asn-68 to Ala-73, Tyr-75 to Met-83, Glu-115 to Leu-140, Ala-144 to Glu-156, Val-159 to Ser-166, Arg-178 to Pro-186, Arg-191 to Ile-198.	AR089: 4, AR061: 2 H0551: 2, H0581: 1, H0560: 1, H0414: 1, S0152: 1 and H0522: 1.	
		908840	538	428 - 757	1151				Ala-54 to Ile-59, His-71 to His-82.		
156	HAUBV06	1106041	166	1164 - 2108	779				Met-5 to Asn-11, Gly-20 to Arg-30, Thr-36 to Ile-41, His-136 to Thr-143, Thr-152 to Asp-161,	AR061: 1, AR089: 0 S0052: 2, S0028: 2, H0624: 1, H0294: 1, S0001: 1, S0282: 1, H0250: 1, H0271: 1,	

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						Gln-70 to Glu-75.	H0305: 1		
		908820	542	50 - 364	1155	Lys-19 to Thr-26.			
159	HDACA35	11107236	169	68 - 913	782	Asp-1 to Lys-12, Pro-18 to Arg-26, Asp-51 to Val-74, Ala-80 to Leu-102.	AR089: 6, AR061: 3 H0497: 1, H0617: 1, L0769: 1, L0766: 1, L0775: 1, H0670: 1 and H0672: 1.		
		908837	543	68 - 460	1156				
160	HDQGM08	1151469	170	541 - 146	783	Glu-25 to Ser-30, Glu-57 to Thr-62, His-64 to Ser-72, His-101 to Pro-106, Val-111 to Gln-117.	AR061: 3, AR089: 2 L0748: 8, H0212: 3, S0010: 2, L0438: 2, L0752: 2, H0170: 1, H0052: 1, H0596: 1, H0051: 1, H0032: 1, H0068: 1, L0800: 1, L0764: 1, L0803: 1, L0791: 1, H0521: 1, L0749: 1, L0758: 1, L0599: 1 and S0192: 1.		
		949210	544	505 - 185	1157	Tyr-7 to Tyr-15, Pro-43 to Ala-52, Gln-57 to Ala-62, Asn-68 to Ala-73, Tyr-75 to Met-83.			
161	HELGB06	11148741	171	287 - 3	784	Gln-38 to Ser-51.	AR089: 2, AR061: 0 S0045: 1 and S0053: 1.		

162	HEOPR74	935730	545	161 - 445	1158	Gln-38 to Ser-51.	AR089: 3, AR061: 2 H0457: 8, H0264: 2, H0645: 1, H0549: 1, H0069: 1, H0599: 1, H0318: 1, H0566: 1, H0132: 1, H0658: 1 and S0350: 1.		
		1226822	172	2 - 937	785	Pro-1 to Gln-8, Lys-32 to Lys-45, Pro-51 to Arg-59, Asp-84 to Val-107, Ala-113 to Leu-135, Gln-137 to Leu-156, Gln-160 to Arg-170, Gln-182 to Pro-194, Lys-201 to Ser-213, Arg-272 to Tyr-278.			
		908836	546	2 - 649	1159	Pro-1 to Gln-8, Lys-32 to Lys-45, Pro-51 to Arg-59, Asp-84 to Val-107, Ala-113 to Leu-135, Gln-137 to Leu-156, Gln-160 to Arg-170, Gln-182 to Leu-198.			
163	HIBEK35	731480	173	3 - 416	786		AR089: 0, AR061: 0 T0010: 2		
164	HUMAR88	1104937	174	3 - 551	787	Ala-11 to Asn-16, Ala-18 to Leu-25, Lys-40 to Arg-52, Tyr-58 to Ile-76, Lys-151 to Thr-162,	AR089: 14, AR061: 5 H0545: 1, H0560: 1 and L0805: 1.		

165	HMWGU56	908839	547	6 - 344	1160	Gln-176 to Gly-182. Ser-11 to Ala-21, Asp-23 to Ile-28.
		1226470	175	800 - 3	788	
		908825	548	3 - 776	1161	Met-16 to Ala-23, Ile-34 to Arg-41, Lys-48 to Pro-54, Leu-65 to Thr-82, Glu-104 to Thr-110, Arg-119 to Tyr-126, Gly-135 to Ala-144, His-153 to His-158.

166	HOUDS09	1164010	176	3 - 1121	789	Asn-178 to Gln-194, Arg-197 to His-202, Ser-236 to Arg-241, Gln-245 to Arg-250.	AR061: 153, AR089: 48 L0599: 12, L0766: 11, L0754: 8, L0803: 2, L0809: 2, L0743: 2, L0731: 2, H0624: 1, H0171: 1, S0040: 1, H0650: 1, H0656: 1, S0298: 1, S0282: 1, H0580: 1, S0046: 1, S0222: 1, H0431: 1, H0587: 1, H0486: 1, S0010: 1, H0318: 1, H0581: 1, H0309: 1, H0416: 1, T0006: 1, H0063: 1, T0041: 1, H0560: 1, S0422: 1, S0002: 1, L0641: 1, L0363: 1, L0523: 1, L0659: 1, H0547: 1, H0539: 1, S0152: 1, H0521: 1, L0758: 1,		
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167	HTEGM38	949051	549	16 - 906	1162	Cys-3 to Glu-8, Gly-13 to Gln-19, Pro-52 to Val-88.	S0242: 1, H0543: 1 and H0423: 1.		
		675087	177	84 - 263	790	Ala-15 to Tyr-24, His-32 to Asp-39.	AR089: 1, AR061: 0 H0038: 2	11q25	602782
168	HTEKY82	1152495	178	499 - 125	791	Gln-85 to Gly-91, Ser-99 to Arg-104.	AR061: 5, AR089: 2 H0038: 3, H0575: 1, H0052: 1, H0628: 1, H0412: 1, L0780: 1 and L0758: 1.		
		908846	550	122 - 517	1163				
169	HTLCY54	1193550	179	1043 - 510	792		AR061: 5, AR089: 5 H0253: 4, H0618: 3, L0758: 3, L0779: 2 and L0794: 1.		
		908832	551	134 - 934	1164	Arg-1 to Arg-6, Ala-49 to Tyr-58, Pro-67 to Lys-80, Ser-92 to Trp-108.			
170	HFOXK14	603245	180	150 - 401	793	Ala-6 to Tyr-17.	AR089: 19, AR061: 8 L0747: 5, L0731: 2, H0656: 1, H0351: 1, H0392: 1, H0333: 1, S0362: 1, S0306: 1,		

								S0002: 1, L0770: 1, L0648: 1, L0776: 1, H0547: 1, H0555: 1 and S0276: 1.			
171	HHFFO69	837703	181	1 - 723	794			AR089: 1, AR061: 1 S0005: 1, H0457: 1, H0009: 1, H0050: 1, S6028: 1, S0036: 1 and H0135: 1.			
172	HHFLU06	857884	182	2 - 328	795			AR061: 5, AR089: 2 H0619: 1			
173	HAGBA56	732597	183	115 - 633	796	Asp-52 to Leu-57, Lys-82 to Thr-87, Ser-90 to Trp-98, Ser-118 to Leu-123.		AR061: 2, AR089: 1 S0010: 1, H0135: 1, L0766: 1, L0745: 1, L0779: 1 and L0758: 1.	7q21-q22	116860, 126650, 126650, 129900, 133170, 154276, 173360, 173360, 602136, 602136, 602136, 602447	
174	HAGGF84	911312	184	1 - 333	797	Lys-14 to Glu-27.		AR061: 3, AR089: 2 L0766: 18, L0748: 11, L0439: 9, L0749: 8,			

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		L0438: 5, L0750: 5, L0777: 4, L0759: 4, H0441: 3, H0052: 3, L0637: 3, L0761: 3, L0740: 3, L0747: 3, L0103: 2, H0574: 2, H0156: 2, H0597: 2, S0250: 2, L0649: 2, L0803: 2, L0806: 2, L0792: 2, S3014: 2, L0757: 2, L0485: 2, L0599: 2, H0171: 1, S6024: 1, L0002: 1, H0657: 1, H0341: 1, S0358: 1, S0360: 1, S0132: 1, L0717: 1, H0632: 1, H0013: 1, H0599: 1, S0010: 1, S0346: 1, H0318: 1, H0251: 1, T0115: 1, H0544: 1, L0471: 1, H0014: 1, S0362: 1, H0083: 1, H0188: 1, H0428: 1, H0646: 1, H0538: 1, L0598: 1, L0762: 1, L0763: 1,					
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175	HAHGD33	921782	185	1 - 1020	798	Phe-22 to Ala-37, Cys-94 to Asn-100, Gly-137 to Pro-145, Glu-172 to Ala-179, Ile-217 to Asp-222.	AR061: 7, AR089: 5 H0039: 5, H0622: 5, L0748: 4, H0667: 4, H0255: 3, S0126: 3, H0393: 2, S0278: 2, H0599: 2, H0618: 2, H0318: 2, H0123: 2, H0050: 2, H0179: 2, H0271: 2, S0036: 2, H0135: 2, H0634: 2, H0087: 2, H0100: 2, H0633: 2, S0210: 2	AR061: 7, AR089: 5 H0039: 5, H0622: 5, L0748: 4, H0667: 4, H0255: 3, S0126: 3, H0393: 2, S0278: 2, H0599: 2, H0618: 2, H0318: 2, H0123: 2, H0050: 2, H0179: 2, H0271: 2, S0036: 2, H0135: 2, H0634: 2, H0087: 2, H0100: 2, H0633: 2, S0210: 2	19p	L0769: 1, L0662: 1, L0768: 1, L0776: 1, L0655: 1, L0659: 1, L0526: 1, L0783: 1, L0789: 1, L0665: 1, S0148: 1, H0520: 1, H0519: 1, S0330: 1, L0602: 1, S0152: 1, S0136: 1, S0350: 1, L0752: 1, H0343: 1, L0366: 1, S0011: 1, H0665: 1, S0196: 1, H0423: 1, L0697: 1 and S0462: 1.
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					S0002: 2, H0144: 2, L0438: 2, L0602: 2, L0744: 2, L0731: 2, L0595: 2, L0601: 2, H0665: 2, H0542: 2, H0556: 1, H0222: 1, H0294: 1, H0583: 1, H0650: 1, H0657: 1, H0484: 1, H0306: 1, S0418: 1, S0420: 1, S0354: 1, H0580: 1, S0007: 1, S0046: 1, H0619: 1, H0550: 1, H0392: 1, H0586: 1, H0333: 1, H0486: 1, H0122: 1, H0196: 1, H0597: 1, H0544: 1, H0009: 1, H0172: 1, L0471: 1, H0023: 1, H0071: 1, H0266: 1, H0290: 1, H0553: 1, H0628: 1, H0551: 1, H0056: 1, H0623: 1, S0038: 1, H0494: 1, H0625: 1, H0561: 1, H0386: 1, H0509: 1,				
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									H0131: 1, H0130: 1, H0646: 1, S0144: 1, S0426: 1, H0529: 1, L0565: 1, H0547: 1, H0689: 1, H0435: 1, H0670: 1, S0330: 1, H0521: 1, S0027: 1, S0028: 1, S0032: 1, L0439: 1, L0747: 1, L0759: 1, S0260: 1, H0445: 1, L0597: 1, L0604: 1, L0593: 1, L0366: 1, H0668: 1, S0242: 1 and H0422: 1.			
176	HAHIY08	962113	186	3 - 278	799				AR061: 10, AR089: 6			
177	HBIOZ10	973131	187	3 - 503	800	Leu-50 to Asp-61, Ser-100 to Leu-107, Ala-120 to Thr-130.			AR054: 189, AR051: 68, AR050: 35, AR089: 4, AR061: 3 H0593: 1			
178	HBKDI30	729048	188	1 - 381	801	Gly-15 to Thr-21, Glu-76 to Lys-86.			AR089: 1, AR061: 0 S0364: 3, S0366: 3, L0604: 3, H0624: 1, L0622: 1, L0623: 1, H0041: 1, L0791: 1, S0380: 1 and L0748: 1.			

179	HBXBW40	706115	189	124 - 456	802	Gln-3 to Ser-12, Arg-33 to Arg-50, Ser-93 to Glu-98.	AR089: 16, AR061: 8 S0038: 2, H0438: 1, S0049: 1 and H0547: 1.		
180	HCEHE35	909937	190	3 - 392	803	Asn-6 to Pro-13.	AR061: 8, AR089: 3 S0222: 1, H0052: 1, H0194: 1, H0290: 1 and H0264: 1.		
181	HCEPW85	911374	191	3 - 314	804	Thr-2 to Gln-7.	H0052: 1 and L0471: 1.		
182	HCFAT25	932068	192	82 - 588	805	Lys-15 to Ser-20, Arg-51 to Arg-60, Lys-64 to Pro-101.	AR061: 2, AR089: 2 S0358: 1, H0413: 1, L0502: 1, L0657: 1, H0522: 1 and H0422: 1.		
183	HCFCF47	1139731	193	3 - 764	806	Leu-1 to Glu-9, Gln-43 to Ala-52, Gly-169 to Gly-176, Arg-178 to Leu-185, Pro-192 to Phe-199.	AR089: 14, AR061: 7 H0341: 1 and H0422: 1.		
		894415	552	2 - 298	1165	Arg-1 to Glu-8.			
184	HDAAV61	810305	194	2 - 343	807	Asp-90 to Lys-105.	AR089: 25, AR061: 11 5q34 L0601: 5, H0266: 4, S0222: 3, H0265: 2, H0556: 2, H0575: 2, H0052: 2, H0271: 2, S0114: 1, S0134: 1, S0420: 1, H0393: 1,	109690, 109690, 123101, 180071, 600584	

					L0757: 3, L0588: 3, S0418: 2, L0618: 2, H0580: 2, L0055: 2, L0769: 2, L0773: 2, L0774: 2, L0791: 2, L0747: 2, L0750: 2, H0265: 1, H0663: 1, S0356: 1, H0208: 1, H0370: 1, H0108: 1, H0575: 1, H0618: 1, H0544: 1, H0545: 1, S0050: 1, H0510: 1, H0286: 1, H0031: 1, H0644: 1, H0068: 1, H0135: 1, L0564: 1, H0494: 1, L0475: 1, H0396: 1, S0144: 1, S0002: 1, S0426: 1, L0763: 1, L0761: 1, L0642: 1, L0764: 1, L0662: 1, L0768: 1, L0806: 1, L0661: 1, L0659: 1, L0367: 1, L0663: 1, H0519: 1, H0435: 1, H0658: 1, S3014: 1, L0751: 1.
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188	HDQDX20	919027	198	210 - 1037	811	Met-7 to Ser-12, Ser-20 to Arg-30, Asp-85 to Ala-92, Met-119 to Asn-146, Pro-151 to Asp-161.	L0749: 1, L0603: 1, H0665: 1 and H0542: 1.		
189	HDQHB19	1226089	199	1 - 747	812	Phe-73 to Pro-81, His-156 to Asp-165, Pro-182 to Lys-187, Lys-196 to Asp-201, Pro-204 to Leu-214, Pro-224 to Asp-231.	AR089: 30, AR061: 4 H0521: 3, H0051: 2, L0756: 2, H0590: 1, S0250: 1, L0772: 1, H0522: 1, S0406: 1 and L0748: 1.		
							AR061: 3, AR089: 3 L0759: 12, L0439: 11, L0766: 7, L0775: 5, H0521: 5, L0755: 5, L0748: 4, L0756: 4, L0777: 4, L0731: 4, L0581: 4, L0619: 3, L0666: 3, L0779: 3, L0757: 3, L0588: 3, S0418: 2, L0618: 2, H0580: 2, L0055: 2, L0769: 2, L0773: 2, L0774: 2, L0791: 2, L0747: 2, L0750: 2, H0265: 1, H0663: 1, S0356: 1, H0208: 1, H0370: 1, H0108: 1, H0575: 1, H0618: 1,		

								H0544: 1, H0545: 1, S0050: 1, H0510: 1, H0286: 1, H0031: 1, H0644: 1, H0068: 1, H0135: 1, L0564: 1, H0494: 1, L0475: 1, H0396: 1, S0144: 1, S0002: 1, S0426: 1, L0763: 1, L0761: 1, L0642: 1, L0764: 1, L0662: 1, L0768: 1, L0806: 1, L0661: 1, L0659: 1, L0367: 1, L0663: 1, H0519: 1, H0435: 1, H0658: 1, S3014: 1, L0751: 1, L0749: 1, L0603: 1, H0665: 1 and H0542: 1.		
190	HDTBY88	934472	895106	553	2 - 538	1166	Pro-14 to Ala-20, Pro-51 to Leu-59, His-67 to Thr-77. His-130 to Lys-140.	AR089: 8, AR061: 2 S0218: 1 and H0486: 1.		
191	HE2KZ07	909948		201	2 - 796	814	Leu-10 to Gly-16, Pro-37 to Glu-45, Glu-78 to Cys-87.	AR061: 9, AR089: 4 H0624: 1		

192	HE8UY74	960914	202	111 - 455	815		AR061: 2, AR089: 1 H0013: 1 and S0027: 1.		
193	HE9NO66	974353	203	362 - 871	816	Phe-8 to Lys-27, Ser-79 to Ser-87, Cys-102 to Val-116.	AR061: 1, AR089: 1 L0774: 2 and H0144: 2.		
194	HEMBT61	939957	204	1 - 351	817		AR061: 8, AR089: 4 L0547: 2, S0046: 1, L0471: 1, L0772: 1, L0529: 1 and L0780: 1.		
195	HETLF29	909762	205	3 - 416	818		AR061: 4, AR089: 2 H0046: 1 and L0758: 1.		
196	HFIUE75	909758	206	2 - 775	819	Cys-1 to Val-10, Ala-14 to Met-22.	AR089: 1, AR061: 1 L0748: 5, S0242: 3, H0615: 2, S0376: 1, S0360: 1, L0717: 1, L0641: 1, L0766: 1, L0664: 1, H0478: 1, L0593: 1 and S0196: 1.		
197	HFKIT06	934019	207	1 - 300	820	Asp-2 to Pro-7, Pro-15 to Gln-20.	AR089: 0, AR061: 0 H0620: 2, L0761: 2, L0766: 2, L0744: 2, L0754: 2, L0596: 2, H0686: 1, H0295: 1, H0657: 1, H0597: 1, H0009: 1, H0264: 1,		

								S0002: 1, L0769: 1, L0774: 1, L0805: 1, L0657: 1, L0790: 1, H0690: 1 and H0521: 1.			
198	HHEGG20	894409	208	26 - 820	821			AR089: 2, AR061: 1 S0360: 1, H0013: 1, L0664: 1 and H0542: 1.			
199	HHEHC53	921783	209	3 - 908	822	Gly-59 to Ser-68, Ala-87 to Glu-98, Pro-106 to Asn-121, Ser-148 to Lys-159, Phe-207 to Ala-222, Ile-284 to Lys-289.		AR089: 3, AR061: 2 L0748: 8, H0039: 5, H0622: 5, L0664: 5, L0439: 5, L0779: 5, L0731: 5, L0758: 5, L0665: 4, L0744: 4, L0601: 4, H0667: 4, H0255: 3, H0618: 3, L0666: 3, L0438: 3, S0126: 3, L0602: 3, L0742: 3, L0604: 3, L0595: 3, H0542: 3, H0265: 2, S0358: 2, H0393: 2, S0278: 2, H0550: 2, H0333: 2, H0599: 2, H0318: 2, H0545: 2, H0123: 2, H0050: 2, H0620: 2, H0179: 2, H0271: 2,	19p		

10^{-10} 10^{-9} 10^{-8} 10^{-7} 10^{-6} 10^{-5} 10^{-4} 10^{-3} 10^{-2} 10^{-1} 10^0 10^1 10^2 10^3 10^4 10^5 10^6 10^7 10^8 10^9 10^{10}

				S0036: 2, H0135: 2, H0634: 2, H0087: 2, H0100: 2, H0633: 2, S0210: 2, S0002: 2, L0769: 2, L0646: 2, L0768: 2, L0774: 2, H0144: 2, L0565: 2, H0689: 2, S0027: 2, L0747: 2, L0755: 2, L0593: 2, H0665: 2, H0556: 1, T0002: 1, H0222: 1, H0685: 1, H0294: 1, S0430: 1, H0583: 1, H0650: 1, H0657: 1, S0212: 1, S0282: 1, H0484: 1, H0306: 1, S0418: 1, S0420: 1, S0354: 1, S0360: 1, H0580: 1, S0007: 1, S0046: 1, H0619: 1, H0351: 1, H0549: 1, H0392: 1, H0586: 1, H0486: 1, T0060: 1, L0022: 1, H0122: 1, H0196: 1, H0597: 1, H0544: 1.				
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									L0753: 1, L0757: 1, L0759: 1, S0260: 1, H0445: 1, H0595: 1, L0597: 1, L0366: 1, H0668: 1, S0242: 1, H0423: 1, H0422: 1 and H0352: 1.		
200	HHERQ79	944057	210	88 - 474	823	Ser-3 to Thr-11, Lys-32 to Gly-39, Thr-50 to Glu-57, Thr-83 to Gln-88.			AR089: 3, AR061: 2 H0597: 1, H0435: 1 and H0543: 1.		
201	HISAF59	959140	211	130 - 843	824	Gly-33 to Ser-48.			AR089: 2, AR061: 2 L0789: 4, L0758: 4, H0657: 3, H0052: 3, H0046: 3, L0438: 3, L0744: 3, L0779: 3, L0005: 2, H0586: 2, H0581: 2, H0194: 2, H0038: 2, L0800: 2, L0659: 2, H0521: 2, L0743: 2, L0439: 2, H0556: 1, S0282: 1, S0358: 1, H0619: 1, H0618: 1, H0231: 1, H0569: 1, S0362: 1, H0622: 1, T0006: 1,		

202	HKAKM10	918685	212	2 - 547	825	Gly-25 to Gln-31, Asn-58 to Leu-63, Lys-71 to His-76, Ile-82 to Arg-88, Ala-134 to Thr-139.	H0135: 1, H0616: 1, H0413: 1, H0623: 1, L0351: 1, S0150: 1, L0769: 1, L0372: 1, L0662: 1, L0794: 1, L0775: 1, L0651: 1, L0527: 1, L0657: 1, L0666: 1, H0144: 1, H0547: 1, H0690: 1, H0658: 1, H0672: 1, H0539: 1, S0378: 1, H0555: 1, L0754: 1, L0747: 1, L0780: 1, L0596: 1, S0192: 1, H0542: 1 and H0423: 1.		
							AR089: 1, AR061: 1 L0794: 4, L0438: 4, L0761: 3, L0766: 3, L0748: 3, L0439: 3, H0556: 2, L0602: 2, L0754: 2, L0779: 2, H0580: 1, H0208: 1, H0013: 1, T0082: 1, S0010: 1, H0428: 1, H0553: 1, H0038: 1, H0616: 1, H0494: 1.		

[illegible]

203	HLTHP86	919354	213	3 - 1310	826			L0796: 1, L0800: 1, L0773: 1, L0533: 1, L0803: 1, L0776: 1, L0657: 1, L0791: 1, H0520: 1, H0519: 1, H0521: 1, H0187: 1, L0731: 1, S0031: 1 and L0366: 1.		
								AR089: 1, AR061: 1 L0439: 3, L0438: 2, S0028: 2, H0656: 1, H0645: 1, H0369: 1, S0222: 1, S0346: 1, H0328: 1, H0029: 1, H0644: 1, H0169: 1, H0591: 1, H0646: 1, H0520: 1, H0539: 1, L0746: 1 and L0366: 1.		
204	HMSJL96	934483	214	1 - 426	827	Thr-15 to Arg-22, Ala-38 to Met-43, Gln-49 to Lys-64, Thr-97 to Gln-108, Thr-131 to Lys-137.		AR054: 16, AR051: 15, AR050: 12, AR089: 0, AR061: 0 L0777: 6, L0758: 5, L0779: 4, L0803: 3, S0358: 2, H0004: 2, L0662: 2, L0775: 2, H0144: 2, S0126: 2.		

	S0328: 2, S3014: 2, S0027: 2, L0743: 2, L0748: 2, H0265: 1, H0656: 1, S0212: 1, H0663: 1, H0638: 1, H0580: 1, H0632: 1, H0486: 1, H0599: 1, H0618: 1, L0105: 1, H0251: 1, H0309: 1, H0544: 1, H0123: 1, H0050: 1, L0471: 1, H0024: 1, H0399: 1, S0003: 1, H0364: 1, H0553: 1, H0038: 1, H0412: 1, H0413: 1, T0041: 1, S0344: 1, S0002: 1, L0598: 1, H0529: 1, L0645: 1, L0363: 1, L0649: 1, L0804: 1, L0805: 1, L0558: 1, L0659: 1, L0528: 1, L0789: 1, L0792: 1, L0666: 1, S0374: 1, H0555: 1, S3012: 1, S0028: 1, S0206: 1, S0032: 1,							
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205	HMTAJ73	813296	215	1 - 438	828	Pro-23 to Lys-28, Gln-39 to Thr-51, Lys-93 to Ala-106, Gln-112 to Pro-129, Pro-132 to Pro-143.	L0439: 1, L0757: 1, S0031: 1, H0707: 1, S0192: 1, H0423: 1, S0042: 1 and H0008: 1. AR061: 24, AR089: 14 L0806: 3, L0772: 2, L0648: 2, H0255: 1, L0717: 1, H0586: 1, H0599: 1, H0618: 1, H0581: 1, H0052: 1, H0123: 1, L0629: 1, L0659: 1, L0663: 1, S0330: 1, H0518: 1 and H0555: 1.			
206	HNTCP13	909770	216	1 - 960	829		AR061: 3, AR089: 2 L0750: 4, H0519: 3, L0666: 2, L0565: 2, H0539: 2, L0742: 2, L0744: 2, L0754: 2, L0777: 2, L0759: 2, H0662: 1, S0045: 1, S0346: 1, H0251: 1, H0030: 1, H0628: 1, H0674: 1, H0529: 1, L0770: 1, L0764: 1, L0526: 1, L0783: 1,	12q12-q13.1	126337, 600194, 600231, 600808, 601284, 601769, 601769, 602116	

									L0787: 1, H0547: 1, H0521: 1, H0696: 1, H0555: 1, L0747: 1, L0749: 1, L0786: 1, L0779: 1, L0780: 1, L0752: 1 and L0592: 1.			
207	HNTMD79	934522	217	182 - 586	830				AR089: 2, AR061: 2 H0519: 2, S0420: 1, T0114: 1, H0013: 1, S0346: 1, H0038: 1, S0142: 1, H0520: 1, H0521: 1 and H0136: 1.			
208	HNTMH70	757184	218	2 - 688	831	Pro-1 to Glu-6, His-17 to Lys-22, Pro-52 to Gln-58.			AR089: 0, AR061: 0 H0520: 1			
209	HNTNB14	909942	219	2 - 658	832	Ala-2 to Gln-9, Arg-22 to Val-29, Glu-51 to Leu-64.			AR089: 1, AR061: 1 S0007: 1, S0222: 1, S0049: 1, L0438: 1, H0520: 1 and L0439: 1.			
210	HODFF88	974911	220	14 - 544	833	His-8 to Gly-18, Glu-150 to Leu-167.			AR054: 34, AR051: 29, AR050: 23, AR089: 4, AR061: 4 H0615: 1			
211	HOHCE47	1216683	221	629 - 2161	834	Tyr-83 to Ser-92, Leu-118 to Tyr-123, Leu-137 to Ser-143,			AR061: 1, AR089: 0 S0040: 1, H0580: 1, S0222: 1, H0355: 1,			

						Gln-148 to Ser-158.	S0250: 1, L0565: 1 and S0152: 1.			
212	HPCRV84	911566	554	1 - 429	1167	Gly-1 to Trp-6.				
		945856	222	112 - 417	835	Thr-1 to Leu-12.	AR089: 0, AR061: 0			
213	HRACK83	888037	223	1 - 471	836	Gln-15 to Gln-21.	AR089: 3, AR061: 2 L0803: 4, L0758: 3, S0212: 2, S0358: 2, H0038: 2, L0770: 2, L0767: 2, L0766: 2, L0748: 2, L0751: 2, L0747: 2, L0759: 2, L0588: 2, L0599: 2, H0411: 1, H0392: 1, H0333: 1, L0021: 1, H0118: 1, T0115: 1, L0471: 1, L0163: 1, H0633: 1, L0769: 1, L0764: 1, L0775: 1, L0376: 1, L0806: 1, L0805: 1, L0807: 1, L0787: 1, H0547: 1, S0122: 1, H0555: 1, H0478: 1, L0744: 1, L0740: 1, L0749: 1, L0750: 1, L0755: 1 and			

214	HRADM45	717358	224	2 - 472	837	Lys-1 to Leu-6, Asp-25 to Pro-30.	L0595: 1. AR089: 14, AR061: 6 H0555: 1 and L0777: 1.		
215	HRAED74	942527	225	289 - 651	838	His-9 to Ile-15.	AR061: 1, AR089: 1 S0222: 3, H0052: 3, L0361: 3, H0179: 2, L0769: 2, H0521: 2, H0555: 2, L0779: 2, L0758: 2, H0663: 1, H0549: 1, S0220: 1, H0586: 1, H0156: 1, S0010: 1, H0596: 1, S0051: 1, T0010: 1, H0271: 1, L0143: 1, H0617: 1, H0652: 1, L0764: 1, L0794: 1, L0806: 1, L0809: 1, H0518: 1, H0478: 1, L0751: 1, L0747: 1, L0750: 1, L0780: 1, L0731: 1 and L0366: 1.		
216	HRODZ70	942673	226	3 - 440	839	Lys-49 to Lys-54, Trp-106 to Lys-112, Leu-130 to Gly-141.	AR089: 12, AR061: 4 H0598: 1 and H0135: 1.		
217	HSKAC24	823869	227	98 - 481	840	Ser-1 to Asp-7,	AR061: 2, AR089: 1		

218	HSSMT34	911294	228	56 - 553	841	Leu-38 to Ser-44, Pro-85 to Tyr-90. Glu-29 to Arg-35, Arg-50 to Leu-55, Leu-60 to Ser-69, Lys-102 to Asp-108, Pro-133 to Gln-141.	AR061: 4, AR089: 3 L0439: 6, L0777: 6, H0052: 4, L0748: 4, H0634: 3, L0662: 3, L0805: 3, L0659: 3, L0438: 3, H0547: 3, L0750: 3, L0758: 3, H0208: 2, H0123: 2, H0014: 2, H0617: 2, H0135: 2, L0769: 2, L0766: 2, L0803: 2, L0776: 2, L0666: 2, L0751: 2, L0745: 2, L0731: 2, H0265: 1, S0408: 1, H0549: 1, H0497: 1, L0622: 1, H0581: 1, H0194: 1, L0738: 1, H0546: 1, H0024: 1, S0362: 1, L0163: 1, T0010: 1, H0083: 1, H0510: 1, H0266: 1, H0428: 1, H0622: 1, H0673: 1, H0598: 1, S0036: 1,	H0370: 2, S0002: 1, S0428: 1 and S0027: 1.		
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									H0163: 1, H0413: 1, L0370: 1, T0041: 1, H0647: 1, L0637: 1, L0667: 1, L0772: 1, L0646: 1, L0800: 1, L0764: 1, L0649: 1, L0657: 1, L0809: 1, L0788: 1, L0663: 1, S0374: 1, H0520: 1, H0670: 1, H0666: 1, S0330: 1, H0539: 1, H0521: 1, H0696: 1, H0478: 1, S0028: 1, L0741: 1, L0747: 1, L0749: 1, L0780: 1, L0752: 1 and H0543: 1.			
219	HT3BG12	921593	229	1 - 381	842	Glu-1 to Ala-15, Lys-25 to Ser-32, Asp-45 to Thr-51, Pro-59 to Pro-65, Pro-78 to Ser-85.			AR061: 8, AR089: 3 L0758: 3, H0159: 2, S0001: 1, H0618: 1, H0660: 1 and L0779: 1.			
220	HTEGO05	932583	230	3 - 884	843	Pro-12 to Tyr-21.			AR089: 1, AR061: 0 H0038: 2, L0745: 2 and H0616: 1.			
221	HTEKT33	953308	231	200 - 1426	844				AR089: 15, AR061: 9 L0766: 4, L0745: 3,			

222	HTEMU66	944419	232	454 - 963	845	Ala-1 to Gln-7, Lys-24 to Ser-30, Pro-44 to Asn-53, Glu-104 to Asp-112, Leu-152 to Ser-157.	AR061: 7, AR089: 5 H0616: 1	L0752: 3, S0360: 2, L0748: 2, L0746: 2, L0755: 2, H0624: 1, S0114: 1, H0098: 1, L0471: 1, H0083: 1, H0428: 1, L0483: 1, H0090: 1, H0616: 1, H0494: 1, H0560: 1, H0509: 1, L0761: 1, L0772: 1, L0803: 1, L0776: 1, L0655: 1, L0792: 1, L0664: 1, S0374: 1, L0438: 1, H0520: 1, H0519: 1, H0435: 1, H0648: 1, S0152: 1, H0521: 1, H0478: 1, L0747: 1, L0756: 1, L0779: 1, L0758: 1, L0759: 1, H0667: 1, H0543: 1 and L0465: 1.			
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223	HTEMV09	909843	233	1 - 711	846	Asp-22 to Asp-28, Leu-98 to Trp-103, Glu-123 to Trp-154.	AR089: 13, AR061: 13 L0666: 3, L0758: 3, H0616: 2, L0779: 2, S0036: 1, L0598: 1, L0766: 1, L0651: 1, L0806: 1, L0776: 1, H0144: 1, H0547: 1, H0672: 1 and H0555: 1.		
224	HTEMV66	1151075	234	861 - 175	847	Ile-39 to Ser-46, Val-69 to Gln-75, Phe-90 to Ser-100.	AR061: 5, AR089: 1 H0616: 1 and L0758: 1.		
		813038	555	1 - 318	1168	Ser-38 to Pro-45.			
225	HTGAU79	1175071	235	62 - 976	848	His-12 to Arg-20, Pro-26 to Asp-43, Ala-62 to Glu-70, Arg-78 to Arg-83, Phe-100 to Gln-105, Gly-129 to Glu-136, Met-182 to Gly-190, Tyr-277 to Ala-284.	AR061: 7, AR089: 4 H0551: 3, H0529: 3, L0769: 3, L0758: 3, S0418: 2, L0770: 2, L0773: 2, L0521: 2, H0701: 2, S0126: 2, L0747: 2, L0731: 2, L0759: 2, L0589: 2, L0601: 2, H0624: 1, H0149: 1, H0556: 1, H0295: 1, S0134: 1, H0583: 1, H0661: 1, H0592: 1, H0013: 1, H0635: 1, H0581: 1,		

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226	HTLEJ11	973302	236	2 - 802	849	His-12 to Arg-20, Pro-26 to Asp-43, Ala-62 to Glu-70, Arg-78 to Arg-83, Phe-100 to Gln-105, Gly-129 to Glu-136.	940369	556	63 - 977	1169	S0250: 1, H0212: 1, H0412: 1, S0144: 1, L0763: 1, L0645: 1, L0764: 1, L0794: 1, L0766: 1, L0775: 1, L0783: 1, L0665: 1, H0519: 1, H0435: 1, H0672: 1, H0436: 1, S3014: 1, S0028: 1, L0750: 1, L0777: 1, L0366: 1, H0667: 1 and H0423: 1.	15q13-qter	
227	HTLIY52	1218691	237	180 - 1376	850	Tyr-52 to Gln-60, Phe-86 to Ala-94, Lys-111 to Arg-118, His-193 to Tyr-198. Pro-3 to Gly-8, Val-21 to Gly-30, Gly-68 to Ala-85, His-94 to Gly-99,	1218691	237	180 - 1376	850	AR061: 3, AR089: 1 H0618: 3 and H0253: 1. AR061: 0, AR089: 0, H0618: 64, H0253: 52, L0758: 6, L0779: 2, H0392: 1, H0038: 1,		

							Ala-105 to Arg-110, Ala-114 to Gln-138, Arg-143 to Glu-155, Leu-202 to Arg-222, Arg-287 to Ser-292, Pro-325 to Arg-332, Arg-337 to Gly-351, Pro-389 to Arg-399.		L0761: 1, L0803: 1, L0806: 1 and L0697: 1.		
		942161	557	1 - 1368	1170						
228	HTOAK34	966800	238	918 - 1196	851		Ser-67 to Trp-77.		AR089: 1, AR061: 1 L0766: 2, H0264: 1 and H0521: 1.		
229	HTPGG25	911282	239	3 - 392	852		Pro-3 to Arg-8.		AR061: 2, AR089: 2 L0439: 6, L0777: 6, H0052: 4, L0748: 4, H0634: 3, L0662: 3, L0805: 3, L0659: 3, L0438: 3, H0547: 3, L0750: 3, L0758: 3, H0208: 2, H0123: 2, H0014: 2, H0617: 2, H0135: 2, L0769: 2, L0766: 2, L0803: 2, L0776: 2, L0666: 2, L0751: 2, L0745: 2, L0731: 2, H0265: 1,		

	S0408: 1, H0549: 1, H0497: 1, L0622: 1, H0581: 1, H0194: 1, L0738: 1, H0546: 1, H0024: 1, S0362: 1, L0163: 1, T0010: 1, H0083: 1, H0510: 1, H0266: 1, H0428: 1, H0622: 1, H0673: 1, H0598: 1, S0036: 1, H0163: 1, H0413: 1, L0370: 1, T0041: 1, H0647: 1, L0637: 1, L0667: 1, L0772: 1, L0646: 1, L0800: 1, L0764: 1, L0649: 1, L0657: 1, L0809: 1, L0788: 1, L0663: 1, S0374: 1, H0520: 1, H0670: 1, H0666: 1, S0330: 1, H0539: 1, H0521: 1, H0696: 1, H0478: 1, S0028: 1, L0741: 1, L0747: 1, L0749: 1, L0780: 1, L0752: 1 and H0543: 1.					
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230	HUJAD24	1161319	240	770 - 1237	853	Gln-49 to Thr-69, His-129 to Cys-143.	AR089: 1, AR061: 0 L0750: 3, H0650: 2, H0637: 2, H0265: 1, H0556: 1, S0222: 1, H0040: 1, H0280: 1, L0655: 1, L0789: 1 and L0666: 1.		
		911498	558	3 - 293	1171				
231	HUTSF11	966029	241	3 - 302	854	Glu-1 to Glu-6, Asn-16 to Arg-22.	AR089: 0, AR061: 0 S0464: 1 and L0356: 1.		
232	HUVGZ88	1227628	242	83 - 862	855	Gln-216 to Asp-226, Thr-250 to Thr-256.	AR089: 2, AR061: 2 L0789: 4, L0758: 4, H0657: 3, H0052: 3, L0438: 3, L0744: 3, L0779: 3, L0005: 2, H0581: 2, H0194: 2, H0046: 2, H0038: 2, L0800: 2, L0659: 2, H0521: 2, L0743: 2, L0439: 2, H0556: 1, S0282: 1, S0358: 1, H0619: 1, H0586: 1, H0618: 1, H0231: 1, S0362: 1, H0622: 1, T0006: 1, H0616: 1, H0413: 1, H0623: 1,		

							L0800: 2, L0659: 2, H0521: 2, L0743: 2, L0439: 2, H0556: 1, S0282: 1, S0358: 1, H0619: 1, H0586: 1, H0618: 1, H0231: 1, S0362: 1, H0622: 1, T0006: 1, H0616: 1, H0413: 1, H0623: 1, L0351: 1, S0150: 1, L0769: 1, L0372: 1, L0662: 1, L0794: 1, L0775: 1, L0651: 1, L0527: 1, L0657: 1, L0666: 1, H0547: 1, H0690: 1, H0658: 1, H0672: 1, H0539: 1, S0378: 1, H0555: 1, L0754: 1, L0747: 1, L0780: 1, L0596: 1, S0192: 1, H0542: 1 and H0423: 1.			
235	HWAFS18	948434	245	54 - 791	858	Pro-1 to Pro-7, Leu-10 to Lys-18, Val-119 to Lys-126, Gln-146 to Trp-151,	AR089: 4, AR061: 3 H0581: 3, H0622: 3, H0575: 2, H0090: 2, L0777: 2, L0757: 2,			

236	HWAGS73	1150212	246	1 - 339	859	Asp-210 to Arg-216.	S0114: 1, H0650: 1, H0255: 1, S0360: 1, S0278: 1, H0486: 1, H0318: 1, H0457: 1, H0039: 1, H0553: 1, L0763: 1, L0761: 1, L0764: 1, L0789: 1, H0144: 1, S0374: 1, S0310: 1, H0555: 1, L0758: 1, H0445: 1 and S0276: 1.		
						Val-14 to Lys-21, Gln-41 to Trp-46, Ala-98 to Pro-103.	AR089: 2, AR061: 2 H0581: 3, H0622: 3, H0575: 2, H0090: 2, L0777: 2, L0757: 2, S0114: 1, H0650: 1, H0255: 1, S0360: 1, S0278: 1, H0486: 1, H0318: 1, H0046: 1, H0457: 1, H0039: 1, H0553: 1, L0763: 1, L0761: 1, L0764: 1, L0789: 1, H0144: 1, S0374: 1, S0310: 1, H0555: 1, L0758: 1, H0445: 1 and S0276: 1.		

		894404	561	1 - 339	1174	Val-14 to Lys-21, Gln-41 to Trp-46, Ala-98 to Pro-103.				
237	HWLEA48	927676	247	100 - 408	860	Pro-1 to Thr-8.	AR089: 1, AR061: 0 S0354: 1 and L0596: 1.			
238	HWLHS82	934505	248	2 - 427	861	Gly-34 to Lys-44, Glu-113 to Glu-118.	AR089: 2, AR061: 1 L0769: 3, S0354: 1, H0393: 1, H0355: 1 and H0124: 1.			
239	HWMIB81	955336	249	1491 - 922	862	Ile-94 to Asp-99, Asp-118 to Pro-123, Glu-131 to Ile-140, Tyr-143 to Asp-152, Glu-169 to Lys-179.	AR061: 1, AR089: 1 L0748: 2, H0171: 1, S0134: 1, S0354: 1, S0358: 1, H0014: 1, H0083: 1, H0510: 1, L0764: 1, L0803: 1, L0789: 1, H0593: 1, H0659: 1, H0539: 1, H0555: 1, L0751: 1, L0758: 1, L0759: 1 and L0595: 1.			
240	HCWDV17	1105673	250	32 - 607	863	Ala-144 to Glu-151, Thr-162 to Thr-168.	AR089: 12, AR061: 6 H0305: 4			
		974478	562	32 - 697	1175	Ala-144 to Glu-151, Thr-162 to Thr-168.				
241	HELDI95	1103374	251	49 - 525	864		AR089: 1, AR061: 1 S0045: 2, S0278: 1,			

									H0191: 1, H0027: 1, H0644: 1, S0028: 1, S0031: 1 and S0260: 1.		
242	HAGFO25	953059	563	461 - 895	1176	Arg-71 to Asp-76.			AR061: 9, AR089: 3 L0794: 11, S0010: 3, S0346: 3, L0791: 2, L0439: 2, L0758: 2, S0222: 1, T0060: 1, H0051: 1, S0388: 1, H0188: 1, S0214: 1, H0252: 1, L0666: 1, L0438: 1, L0743: 1, L0750: 1, L0779: 1, S0031: 1, L0480: 1, L0597: 1 and H0667: 1.		
		1150845	252	1 - 735	865	Gly-1 to Glu-7, Gly-30 to Gln-40, Gly-69 to Gln-75, Leu-98 to Leu-107, Tyr-146 to Gly-161, Arg-179 to Ser-186.					
		957992	564	3 - 728	1177	Gly-26 to Gln-36, Gly-65 to Gln-71, Leu-94 to Leu-103.					
243	HAWAB54	1149319	253	1440 - 283	866	Ala-16 to Thr-21, Arg-76 to Asn-104, Ala-123 to Glu-129, Leu-142 to Glu-147, Gly-170 to Gln-180, Gly-209 to Gln-215, Leu-238 to Leu-247,			L0794: 11, S0010: 3, S0346: 3, L0791: 2, L0439: 2, L0758: 2, S0222: 1, T0060: 1, H0051: 1, S0388: 1, H0188: 1, S0214: 1, H0252: 1, L0666: 1,		

Year	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100																																																		
Population	1000000	1050000	1100000	1150000	1200000	1250000	1300000	1350000	1400000	1450000	1500000	1550000	1600000	1650000	1700000	1750000	1800000	1850000	1900000	1950000	2000000	2050000	2100000	2150000	2200000	2250000	2300000	2350000	2400000	2450000	2500000	2550000	2600000	2650000	2700000	2750000	2800000	2850000	2900000	2950000	3000000	3050000	3100000	3150000	3200000	3250000	3300000	3350000	3400000	3450000	3500000	3550000	3600000	3650000	3700000	3750000	3800000	3850000	3900000	3950000	4000000	4050000	4100000	4150000	4200000	4250000	4300000	4350000	4400000	4450000	4500000	4550000	4600000	4650000	4700000	4750000	4800000	4850000	4900000	4950000	5000000	5050000	5100000	5150000	5200000	5250000	5300000	5350000	5400000	5450000	5500000	5550000	5600000	5650000	5700000	5750000	5800000	5850000	5900000	5950000	6000000	6050000	6100000	6150000	6200000	6250000	6300000	6350000	6400000	6450000	6500000	6550000	6600000	6650000	6700000	6750000	6800000	6850000	6900000	6950000	7000000	7050000	7100000	7150000	7200000	7250000	7300000	7350000	7400000	7450000	7500000	7550000	7600000	7650000	7700000	7750000	7800000	7850000	7900000	7950000	8000000	8050000	8100000	8150000	8200000	8250000	8300000	8350000	8400000	8450000	8500000	8550000	8600000	8650000	8700000	8750000	8800000	8850000	8900000	8950000	9000000	9050000	9100000	9150000	9200000	9250000	9300000	9350000	9400000	9450000	9500000	9550000	9600000	9650000	9700000	9750000	9800000	9850000	9900000	9950000	10000000

244	HLIBV06	957993	565	9 - 374	1178	Arg-1 to Arg-6.	Tyr-286 to Gly-301, Arg-319 to Ser-326.	L0438: 1, L0743: 1, L0750: 1, L0779: 1, S0031: 1, L0480: 1, L0597: 1 and H0667: 1.		
		934887	254	3 - 350	867	Arg-1 to Thr-6, Pro-8 to Arg-24, Glu-30 to Lys-35.		AR089: 4, AR061: 2 L0752: 13, L0777: 10, H0663: 7, L0803: 7, L0731: 7, S0356: 6, H0441: 6, L0766: 6, L0758: 6, L0646: 5, L0659: 5, L0485: 5, H0586: 4, H0031: 4, H0553: 4, L0521: 4, L0664: 4, H0660: 4, S0378: 4, L0740: 4, L0754: 4, L0756: 4, H0431: 3, H0615: 3, H0673: 3, S0040: 2, S0354: 2, S0360: 2, H0369: 2, H0331: 2, T0040: 2, H0318: 2, L0471: 2, H0197: 2, H0428: 2, L0770: 2, L0662: 2, L0774: 2, L0651: 2, L0666: 2,		

[illegible]

		S0374: 2, S0126: 2, H0518: 2, H0555: 2, L0747: 2, L0750: 2, L0759: 2, S0031: 2, L0591: 2, H0506: 2, H0352: 2, L0615: 1, H0685: 1, S0114: 1, S0358: 1, S0376: 1, H0637: 1, H0580: 1, H0411: 1, H0592: 1, H0632: 1, T0039: 1, S0280: 1, H0156: 1, L0021: 1, H0599: 1, H0098: 1, T0048: 1, S0474: 1, H0421: 1, H0251: 1, H0263: 1, H0596: 1, H0597: 1, H0231: 1, H0009: 1, H0199: 1, H0246: 1, H0057: 1, H0014: 1, H0355: 1, H0510: 1, H0379: 1, H0059: 1, H0494: 1, S0464: 1, S0466: 1, H0509: 1, H0641: 1, H0647: 1, L0369: 1, L0772: 1,					
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245	HMALL66	1105097	255	38 - 376	868	Gln-54 to Val-63, Asn-88 to Pro-93.	AR061: 9, AR089: 3 L0770: 4, H0638: 1, S0278: 1, H0641: 1, L0763: 1, L0809: 1, L0779: 1 and L0758: 1.	L0771: 1, L0804: 1, L0805: 1, L0776: 1, L0657: 1, L0382: 1, L0809: 1, L0663: 1, L0665: 1, H0144: 1, H0691: 1, T0068: 1, H0520: 1, H0658: 1, H0648: 1, H0539: 1, H0521: 1, S0028: 1, L0744: 1, L0748: 1, L0779: 1, L0592: 1, L0604: 1, L0362: 1 and S0276: 1.		
		956195	566	39 - 377	1179	Gln-54 to Val-63, Asn-88 to Pro-93.				
246	HOACE12	858976	256	2 - 349	869		AR089: 2, AR061: 1 L0794: 11, S0010: 3, S0346: 3, L0791: 2, L0439: 2, L0758: 2, S0222: 1, T0060: 1, H0051: 1, S0388: 1,			

									H0188: 1, S0214: 1, H0252: 1, L0666: 1, L0438: 1, L0743: 1, L0750: 1, L0779: 1, S0031: 1, L0480: 1, L0597: 1 and H0667: 1.		
247	HOGCG69	924848	257	480 - 1187	870	Asn-29 to Gly-39, Pro-49 to Asn-56, Gln-112 to Ala-119, Arg-193 to Gln-201, Leu-222 to Gln-227.			AR089: 36, AR061: 2 H0616: 2, H0618: 1, H0604: 1, H0063: 1 and H0435: 1.		
248	HAGAE09	1150864	258	852 - 565	871	Ser-47 to His-52.			AR061: 1, AR089: 1 L0005: 1, H0438: 1, S0010: 1, L0665: 1, H0444: 1 and L0594: 1.		
249	HAGAE34	1121869	259	48 - 206 193 - 480	872	Leu-16 to Ser-32. Phe-7 to Glu-13, Gln-46 to Thr-59.			AR089: 10, AR061: 8 L0439: 2, S0010: 1, L0796: 1 and L0805: 1.		
250	HARMH78	1137572	260	83 - 322 560 - 3	873				AR089: 13, AR061: 5 S0360: 1, H0592: 1 and H0087: 1.		
251	HBJLB53	1226988	261	87 - 284 1150 - 869	874	Gln-24 to Arg-44. Asn-8 to Thr-14, Gly-38 to Gly-44,			AR089: 9, AR061: 8 H0318: 2, H0171: 1,		

						Lys-58 to Val-63, Tyr-71 to Val-78.	H0069: 1, H0123: 1, L0783: 1, H0521: 1 and L0748: 1.		
						Gln-20 to Arg-26.	AR061: 4, AR089: 4 H0318: 1, L0766: 1 and L0748: 1.		
252	HBJNB52	974122	570	298 - 450	1183	Leu-16 to Glu-22, Tyr-89 to Asn-95.	AR089: 4, AR061: 2 L0163: 3, H0497: 2, L0439: 2, H0662: 1, S0360: 1, L0717: 1, S6016: 1, S0051: 1, H0428: 1, L0662: 1, L0768: 1, L0774: 1, L0776: 1, L0656: 1, L0789: 1, L0666: 1, L0743: 1, L0749: 1 and L0777: 1.		
						Pro-15 to Cys-23.			
253	HDABQ83	726475	571	160 - 357	1184	Lys-17 to Phe-26, Gln-30 to Leu-43.			
		1201703	263	183 - 1	876				
254	HDPDC84	669619	572	219 - 374	1185	Asp-3 to Ser-11.	AR061: 4, AR089: 1 L0749: 6, L0794: 5, H0550: 4, H0575: 4, H0521: 4, L0601: 4, H0580: 3, L0761: 3, L0766: 3, H0402: 2,		
		1226990	264	82 - 2970	877	Lys-32 to Val-61, Pro-83 to Ala-89, Lys-114 to Gly-120, Asn-137 to Arg-147, Gly-186 to Thr-194, Val-211 to Glu-227,			

Ile-236 to Glu-242, Phe-254 to Lys-264, Glu-328 to Leu-334, Phe-355 to Asn-379, Thr-434 to Leu-444, Glu-495 to Leu-502, Gln-533 to Lys-538, Ser-586 to Trp-594, Leu-605 to Glu-611, Pro-614 to Leu-624, Thr-626 to Gln-640, Ser-679 to Ala-684, Lys-750 to Gly-771, Glu-840 to Asp-853, Glu-866 to Glu-874, Ser-881 to Ala-915, Asn-929 to Gly-944, Ala-946 to Thr-953.	S0360: 2, H0549: 2, H0628: 2, H0264: 2, H0560: 2, S0002: 2, L0803: 2, L0787: 2, L0789: 2, S3014: 2, L0777: 2, L0752: 2, L0731: 2, H0423: 2, H0657: 1, S0212: 1, H0306: 1, H0589: 1, S0358: 1, S0046: 1, H0610: 1, H0391: 1, H0486: 1, H0250: 1, S0280: 1, H0318: 1, H0581: 1, H0309: 1, H0373: 1, H0030: 1, H0135: 1, H0038: 1, H0634: 1, H0272: 1, H0494: 1, H0509: 1, S0426: 1, L0662: 1, L0804: 1, L0775: 1, L0806: 1, L0659: 1, L0532: 1, H0547: 1, H0555: 1, S0432: 1, L0754: 1, L0747: 1, L0750: 1, L0779: 1, L0758: 1, S0031: 1,
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256	HDPWU07	1228286	266	1036 - 1416	879	Ala-9 to Glu-20, Thr-22 to Gly-32, Gly-57 to Ser-67, Arg-125 to Ser-138, Gly-167 to Gln-176. Ser-77 to His-82.	970586	574	49 - 705	1187	H0458: 1, S0140: 1, H0550: 1, H0497: 1, H0575: 1, S0474: 1, H0421: 1, H0024: 1, H0213: 1, H0087: 1, H0272: 1, H0641: 1, S0144: 1, L0763: 1, L0761: 1, L0662: 1, L0794: 1, L0803: 1, L0804: 1, L0659: 1, L0787: 1, L0666: 1, L0663: 1, H0518: 1, S0044: 1, H0576: 1, L0756: 1, H0422: 1, S0452: 1 and H0506: 1.	AR089: 2, AR061: 1 H0587: 3, L0664: 3, L0665: 3, H0648: 3, L0740: 3, H0581: 2, L0659: 2, H0539: 2, H0521: 2, L0750: 2,
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									L0777: 2, L0759: 2, H0423: 2, S0218: 1, H0661: 1, H0305: 1, H0459: 1, S0360: 1, H0580: 1, L0717: 1, H0486: 1, T0074: 1, H0036: 1, H0051: 1, S0388: 1, H0039: 1, H0553: 1, H0124: 1, H0412: 1, L0770: 1, L0662: 1, L0768: 1, L0766: 1, L0649: 1, L0775: 1, L0789: 1, L0791: 1, L0532: 1, S0216: 1, H0682: 1, H0659: 1, H0670: 1, S0270: 1, H0540: 1, L0747: 1, L0780: 1, L0755: 1, L0592: 1, L0581: 1, L0604: 1 and H0422: 1.					
257	HDTJJ02	952734	575	297 - 446	1188	Pro-47 to Gly-54.	AR089: 34, AR061: 11 H0486: 2							
		1106328	267	86 - 331	880									
		913787	576	3 - 116	1189									
258	HE2GA18	1121872	268	288 - 1	881	Tyr-1 to Ser-10,	AR089: 1, AR061: 1							

[illegible]

						Gln-19 to Glu-27.		H0171: 1, H0383: 1 and S0028: 1.		
		867276	577	2 - 160	1190					
259	HE2SY03	1207925	269	1084 - 725	882	Val-10 to Ser-22, Ile-26 to Ser-46, Thr-86 to Asn-91, His-110 to Asn-119.		AR089: 6, AR061: 4, L0749: 2 and H0624: 1.		
		947947	578	195 - 455	1191	Ser-7 to Ile-14, His-48 to Gln-54, His-68 to His-74, Pro-80 to His-87.				
260	HELGY64	1228289	270	1 - 2463	883	Asn-129 to Ser-140, Glu-164 to Thr-169, Leu-173 to Ser-184, Ala-186 to Arg-192, Lys-239 to Ala-250, Asp-285 to Gly-291, Ser-305 to Gln-316, Thr-334 to Glu-344, Tyr-350 to Asp-365, Gln-373 to Lys-382, Pro-429 to Gly-434, Gly-510 to Arg-518, Pro-531 to Arg-539, Glu-585 to Leu-593, Gln-669 to Ser-674,	AR061: 3, AR089: 3 L0751: 10, L0743: 9, H0556: 4, S0046: 3, L0662: 3, L0779: 3, H0265: 2, S0045: 2, H0581: 2, H0355: 2, H0271: 2, H0030: 2, H0063: 2, S0002: 2, H0529: 2, L0372: 2, L0659: 2, L0602: 2, S0404: 2, L0756: 2, L0605: 2, H0423: 2, S0114: 1, H0650: 1, H0656: 1, L0785: 1, S0212: 1, H0663: 1,			

[illegible]

									S0002: 1, L0631: 1, L0769: 1, L0372: 1, L0764: 1, L0768: 1, L0803: 1, L0783: 1, L0545: 1, L0791: 1, L0664: 1, L0665: 1, H0144: 1, L0438: 1, H0689: 1, S0380: 1, S0013: 1, H0696: 1, H0555: 1, L0743: 1, L0744: 1, L0747: 1, L0731: 1, L0759: 1, L0596: 1 and L0604: 1.		
262	HFVIP88	697730	580	2 - 181	1193	Gly-43 to Tyr-50.			AR061: 6, AR089: 2 L0755: 5, H0212: 2, L0439: 2, L0754: 2, H0393: 1, H0409: 1, L0764: 1, L0662: 1, L0803: 1, L0382: 1, L0666: 1, L0438: 1, L0749: 1 and L0752: 1.		
263	HGBAS76	960741	581	96 - 299	1194						
		1193040	273	1181 - 1603	886	Asn-36 to Gly-43, Gly-66 to Glu-73, Ser-86 to Pro-92,			AR089: 1, AR061: 0 L0747: 5, L0439: 3, L0756: 3, L0775: 2,		

						Asn-124 to Leu-133.				L0755: 2, L0759: 2, S0342: 1, S6024: 1, S0376: 1, L0021: 1, H0150: 1, T0003: 1, H0014: 1, L0764: 1, L0794: 1, L0803: 1, L0783: 1, L0809: 1, L0666: 1, L0665: 1, L0438: 1, L0749: 1, L0779: 1, L0777: 1, L0758: 1, L0604: 1, S0026: 1 and H0423: 1.		
264	HHEBB62	771320	582	274 - 426	1195	Asn-18 to Arg-23.				AR089: 7, AR061: 3 L0731: 3, H0395: 2, L0764: 2, L0794: 2, H0521: 2, T0049: 1, H0650: 1, S0140: 1, L0021: 1, H0083: 1, H0271: 1, L0769: 1, L0761: 1, L0646: 1, L0771: 1, L0803: 1, L0804: 1, L0775: 1, L0519: 1, H0445: 1, L0588: 1 and H0542: 1.		
		1151481	274	459 - 1	887	Ser-47 to Thr-54, Asn-62 to Asp-67, Pro-109 to Ser-114, Arg-146 to Arg-153.						
		791469	583	529 - 158	1196	Pro-27 to Lys-34,						

265	HHEHU73	1151483	275	378 - 746	888	Glu-49 to Asn-59, Lys-70 to Lys-82, Gly-99 to Cys-116.	AR089: 64, AR061: 15 H0542: 2		
		923895	584	61 - 279	1197	Glu-4 to Leu-11, Gln-30 to Cys-40, Pro-53 to Pro-59, Thr-99 to Ser-104.			
266	HHEMA11	1151484	276	129 - 497	889	Gln-13 to Ile-29.	AR089: 3, AR061: 1 H0328: 1, L0758: 1 and H0543: 1.		
		966924	585	129 - 497	1198	Gln-13 to Ile-29.			
267	HHEQK01	1107392	277	195 - 1	890	Gln-1 to Thr-6.	AR089: 7, AR061: 1 L0589: 1, H0542: 1 and H0543: 1.		
		871911	586	64 - 249	1199				
268	HHPEM84	915639	278	2 - 373	891		AR089: 68, AR061: 29	20q11.2-q12	139190, 139190, 224100, 600281, 600281, 601002, 601002, 601146, 601146, 601146

269	HHSED84	1150832	279	632 - 3	892	Asp-73 to Ser-80, Arg-104 to Asp-115, Glu-195 to Pro-202.	AR061: 8, AR089: 4 L0748: 5, L0744: 4, L0751: 4, H0039: 3, H0617: 3, L0646: 3, L0809: 3, L0779: 3, H0295: 2, H0255: 2, S0358: 2, H0575: 2, H0457: 2, H0181: 2, H0673: 2, L0637: 2, L0743: 2, L0750: 2, L0758: 2, S0116: 1, H0663: 1, S0356: 1, S0376: 1, S0360: 1, H0675: 1, S0007: 1, H0497: 1, H0590: 1, H0618: 1, H0253: 1, H0545: 1, S0051: 1, H0622: 1, H0030: 1, H0135: 1, H0538: 1, S0426: 1, H0529: 1, L0763: 1, L0769: 1, L0764: 1, L0771: 1, L0773: 1, L0775: 1, L0788: 1, L0663: 1, H0144: 1, L0438: 1, H0690: 1, H0670: 1,		
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270	HIBCC94	706739	587	2 - 496	1200	Asn-1 to Asp-8, Gly-51 to Ser-64.	H0672: 1, S0328: 1, S0406: 1, H0187: 1, L0747: 1, L0749: 1, L0759: 1 and L0608: 1.		
		1161292	280	806 - 258	893	Cys-12 to Gln-17, Lys-47 to Thr-57, Leu-77 to Gly-92, Gln-153 to Arg-160.			
		504326	588	3 - 251	1201	Glu-1 to Arg-6, Ser-11 to Val-17, Gln-42 to Arg-54.			
		504330	589	470 - 132	1202				
271	HKADN56	1220254	281	370 - 1650	894	Ser-32 to Glu-39, Ala-60 to Trp-69.	AR089: 7, AR061: 4 L0754: 12, S0360: 8, S0152: 7, S0358: 6, H0046: 6, H0100: 5, L0751: 5, L0777: 5, L0601: 5, H0052: 4, L0740: 4, H0051: 3, H0266: 3, L0526: 3, S0374: 3, L0779: 3, H0265: 2, H0556: 2, H0341: 2, H0661: 2, H0619: 2, H0050: 2,		

					H0188: 1, H0290: 1, H0252: 1, H0328: 1, H0424: 1, H0213: 1, H0031: 1, H0553: 1, H0032: 1, H0674: 1, H0361: 1, H0135: 1, H0038: 1, H0551: 1, H0264: 1, H0412: 1, H0059: 1, H0494: 1, H0561: 1, S0142: 1, S0344: 1, S0210: 1, S0002: 1, L0769: 1, L0644: 1, L0773: 1, L0767: 1, L0766: 1, L0776: 1, L0542: 1, L0783: 1, L0382: 1, L0530: 1, L0367: 1, L0790: 1, L0666: 1, L0663: 1, L0664: 1, L0665: 1, H0144: 1, H0520: 1, H0547: 1, H0593: 1, H0666: 1, H0696: 1, H0436: 1, L0747: 1, L0749: 1, L0757: 1, H0445: 1, H0707: 1, L0596: 1,
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									L0593: 1, S0011: 1, H0668: 1, H0542: 1, H0423: 1, H0422: 1, S0456: 1 and H0352: 1.		
272	HKIXG58	968619	590	3 - 257	1203	Lys-11 to Ala-39, Ser-52 to Asp-57.			AR061: 2, AR089: 2 H0441: 3, L0794: 2, L0805: 2, L0764: 1 and L0521: 1.		
273	HLICI13	464241	591	3 - 200	1204	Ser-9 to Lys-14.			AR089: 3, AR061: 1 L0439: 4, L0769: 2, L0662: 2, L0592: 2, S0046: 1, H0618: 1, H0545: 1, S0388: 1, S0051: 1, H0355: 1, H0264: 1, H0561: 1, L0770: 1, L0372: 1, L0508: 1, H0547: 1, H0689: 1, L0731: 1 and L0758: 1.		
274	HLTGF17	626559	592	205 - 510	1205	Arg-151 to Thr-159, Arg-168 to Lys-173, Glu-181 to His-190, Phe-237 to Asn-242, Asp-267 to Glu-274, Tyr-283 to Pro-300, Pro-306 to Trp-311, Ala-371 to Asp-383.			AR061: 7, AR089: 6 L0766: 4, H0620: 3, L0663: 3, L0749: 3,		
		662405	284	1 - 234	897	Pro-16 to Leu-22, Arg-32 to Gln-37, Thr-55 to Thr-72.					

No.	Name	Age	Height		Weight		Chest		Arm		Forearm		Hand		Foot		Ankle		Knee		Hip		Shoulder		Elbow		Wrist		Neck		Head		Face		Eyes		Ears		Nose		Mouth		Teeth		Tongue		Throat		Larynx		Trachea		Esophagus		Stomach		Intestine		Liver		Spleen		Pancreas		Gallbladder		Bladder		Uterus		Vagina		Penis		Prostate		Testis		Scrotum		Penile		Vaginal		Rectum		Sigmoid		Colon		Rectal		Anal		Urethra		Uterine		Fallopian		Ovary		Vulva		Clitoris		Labia		Perineum		Anus		Rectal		Sigmoid		Colon		Rectal		Anal		Urethra		Uterine		Fallopian		Ovary		Vulva		Clitoris		Labia		Perineum		Anus		Rectal		Sigmoid		Colon		Rectal		Anal		Urethra		Uterine		Fallopian		Ovary		Vulva		Clitoris		Labia		Perineum		Anus		Rectal		Sigmoid		Colon		Rectal		Anal		Urethra		Uterine		Fallopian		Ovary		Vulva		Clitoris		Labia		Perineum		Anus		Rectal		Sigmoid		Colon		Rectal		Anal		Urethra		Uterine		Fallopian		Ovary		Vulva		Clitoris		Labia		Perineum		Anus		Rectal		Sigmoid		Colon		Rectal		Anal		Urethra		Uterine		Fallopian		Ovary		Vulva		Clitoris		Labia		Perineum		Anus		Rectal		Sigmoid		Colon		Rectal		Anal		Urethra		Uterine		Fallopian		Ovary		Vulva		Clitoris		Labia		Perineum		Anus		Rectal		Sigmoid		Colon		Rectal		Anal		Urethra		Uterine		Fallopian		Ovary		Vulva		Clitoris		Labia		Perineum		Anus		Rectal		Sigmoid		Colon		Rectal		Anal		Urethra		Uterine		Fallopian		Ovary		Vulva		Clitoris		Labia		Perineum		Anus		Rectal		Sigmoid		Colon		Rectal		Anal		Urethra		Uterine		Fallopian		Ovary		Vulva		Clitoris		Labia		Perineum		Anus		Rectal		Sigmoid		Colon		Rectal		Anal		Urethra		Uterine		Fallopian		Ovary		Vulva		Clitoris		Labia		Perineum		Anus		Rectal		Sigmoid		Colon		Rectal		Anal		Urethra		Uterine		Fallopian		Ovary		Vulva		Clitoris		Labia		Perineum		Anus		Rectal		Sigmoid		Colon		Rectal		Anal		Urethra		Uterine		Fallopian		Ovary		Vulva		Clitoris		Labia		Perineum		Anus		Rectal		Sigmoid		Colon		Rectal		Anal		Urethra		Uterine		Fallopian		Ovary		Vulva		Clitoris		Labia		Perineum		Anus		Rectal		Sigmoid		Colon		Rectal		Anal		Urethra		Uterine		Fallopian		Ovary		Vulva		Clitoris		Labia		Perineum		Anus		Rectal		Sigmoid		Colon		Rectal		Anal		Urethra		Uterine		Fallopian		Ovary		Vulva		Clitoris		Labia		Perineum		Anus		Rectal		Sigmoid		Colon		Rectal		Anal		Urethra		Uterine		Fallopian		Ovary		Vulva		Clitoris		Labia		Perineum		Anus		Rectal		Sigmoid		Colon		Rectal		Anal		Urethra		Uterine		Fallopian		Ovary		Vulva		Clitoris		Labia		Perineum		Anus		Rectal		Sigmoid		Colon		Rectal		Anal		Urethra		Uterine		Fallopian		Ovary		Vulva		Clitoris		Labia		Perineum		Anus		Rectal		Sigmoid		Colon		Rectal		Anal		Urethra		Uterine		Fallopian		Ovary		Vulva		Clitoris		Labia		Perineum		Anus		Rectal		Sigmoid		Colon		Rectal		Anal		Urethra		Uterine		Fallopian		Ovary		Vulva		Clitoris		Labia		Perineum		Anus		Rectal		Sigmoid		Colon		Rectal		Anal		Urethra		Uterine		Fallopian		Ovary		Vulva		Clitoris		Labia		Perineum		Anus		Rectal		Sigmoid		Colon		Rectal		Anal		Urethra		Uterine		Fallopian		Ovary		Vulva		Clitoris	
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275	HLYDC50	1151494	285	2 - 874	898	Ser-1 to Ser-10, Ser-23 to Asp-38, Arg-67 to Lys-73, Ser-181 to Asp-187, Asp-222 to Ser-233, Pro-248 to Asn-253.	AR061: 4, AR089: 3, L0766: 5, L0806: 3, T0010: 2, L0761: 2, L0752: 2, H0677: 2, S0278: 1, H0486: 1, S0038: 1, L0796: 1,	AR061: 4, AR089: 3, L0766: 5, L0806: 3, T0010: 2, L0761: 2, L0752: 2, H0677: 2, S0278: 1, H0486: 1, S0038: 1, L0796: 1,	
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									L0644: 1, L0771: 1, L0659: 1, L0666: 1, L0664: 1, H0521: 1, L0779: 1, H0445: 1 and L0595: 1.		
		677050	593	2 - 424	1206	Ser-1 to Ser-10, Ser-23 to Asp-38.					
276	HMADD49	1217031	286	2227 - 803	899	Pro-45 to Ser-50, Thr-54 to Ile-64, Lys-205 to Arg-211, Pro-214 to Gly-220, Asp-296 to Asp-301, Pro-355 to Glu-367, Thr-391 to Glu-396.			AR061: 77, AR089: 30 S0136: 3, S0036: 1 and S0144: 1.		
		867481	594	2 - 283	1207	Leu-33 to Phe-38.					
277	HMEKE78	1128290	287	80 - 1339	900	Pro-39 to Glu-45, Pro-102 to Arg-107, Tyr-121 to Lys-128, Gln-140 to Ile-169, Arg-269 to Gly-285, Lys-313 to Gly-320, Ala-344 to Thr-350, Arg-356 to Gln-365, Tyr-373 to His-380, Arg-392 to Leu-399, Leu-403 to Gln-408.			AR061: 10, AR089: 5 S0328: 4, S0218: 3, H0040: 2, L0438: 2, L0439: 2, H0624: 1, H0431: 1, L0021: 1, S0049: 1, H0266: 1, H0090: 1, H0561: 1, S0422: 1, H0529: 1, L0659: 1, S0126: 1, S0027: 1, S0028: 1, S0206: 1, L0748: 1,		

278	HMSHU26	792383	595	3 - 461	1208	Phe-3 to Phe-8, Pro-30 to Glu-36, Pro-93 to Arg-98.	L0731: 1, S0031: 1, L0596: 1, L0608: 1 and S0011: 1.		
		1150833	288	993 - 703	901	Ser-41 to Glu-47, Arg-71 to Leu-85, Asp-87 to Glu-97.			
279	HNEEB82	681745	596	29 - 235	1209	Glu-15 to His-24, Asn-47 to His-53.	AR061: 5, AR089: 4 L0748: 2, H0191: 1, H0100: 1, S0002: 1, L0646: 1, L0794: 1, L0806: 1 and L0758: 1.		
		1076509	289	261 - 1	902	Gln-1 to Gly-7, Ser-63 to Gly-68, Pro-74 to Cys-81.			
280	HNHIA06	778884	597	30 - 260	1210	Glu-1 to Glu-22.	AR061: 5, AR089: 3 L0766: 2, H0575: 1, H0179: 1, H0416: 1, H0539: 1 and L0592: 1.		
		1162086	290	605 - 159	903	Asp-29 to Arg-35, Leu-58 to Thr-64.			
281	HODFY16	859932	598	120 - 566	1211	Asp-29 to Arg-35, Leu-58 to Thr-64.	AR089: 3, AR061: 3 S0282: 1 and S0053: 1.		
		1105244	291	370 - 221	904	Ile-34 to Gly-42.			
		958329	599	163 - 309	1212		AR061: 6, AR089: 3 H0615: 2 and L0766: 1.		

282	HPQSB68	1221022	292	294 - 97	905	Asp-36 to Lys-42.	AR089: 1, AR061: 1 S0136: 2			
		740087	600	89 - 247	1213	Leu-7 to Gln-17.				
283	HRDBH04	1150876	293	329 - 724	906	Thr-56 to Gly-62, Glu-72 to Gly-81.	AR089: 7, AR061: 6 L0769: 16, L0776: 16, L0742: 13, L0745: 13, L0754: 12, L0748: 11, L0439: 11, L0747: 10, L0805: 8, L0438: 6, L0731: 6, L0764: 5, L0806: 5, L0749: 5, L0779: 5, L0752: 5, L0771: 4, H0052: 3, L0796: 3, L0761: 3, L0741: 3, L0756: 3, L0753: 3, L0758: 3, S0360: 2, H0013: 2, H0068: 2, T0041: 2, L0768: 2, L0659: 2, L0783: 2, L0809: 2, H0670: 2, L0746: 2, L0591: 2, H0265: 1, H0686: 1, H0583: 1, H0657: 1, L0785: 1, H0662: 1, S0418: 1,			

	S0132: 1, S0222: 1, H0441: 1, H0455: 1, L0622: 1, H0486: 1, T0039: 1, H0036: 1, S0010: 1, H0544: 1, H0545: 1, H0123: 1, H0024: 1, T0010: 1, H0615: 1, H0622: 1, T0006: 1, H0604: 1, H0424: 1, H0213: 1, H0401: 1, H0182: 1, H0617: 1, H0124: 1, H0038: 1, H0488: 1, H0623: 1, H0059: 1, S0112: 1, H0494: 1, L0475: 1, H0334: 1, H0560: 1, L0640: 1, L0770: 1, L0630: 1, L0773: 1, L0766: 1, L0774: 1, L0775: 1, L0655: 1, L0807: 1, L0527: 1, L0788: 1, L0789: 1, L0666: 1, H0593: 1, H0682: 1, H0659: 1, H0660: 1, H0666: 1, S0380: 1,					
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									L0743: 1, L0777: 1, L0780: 1, L0755: 1, L0757: 1, L0759: 1, L0603: 1, S0026: 1, H0543: 1 and H0352: 1.		
284	HSICR69	922022	601	285 - 680	1214	Thr-56 to Gly-62, Glu-72 to Gly-81.			AR089: 2, AR061: 1 H0036: 2		
285	HSIGJ94	1226965	294	547 - 29	907	Thr-48 to Arg-54, Pro-149 to Ser-155.			AR061: 8, AR089: 7 H0590: 1, L0766: 1, L0659: 1, L0608: 1 and L0362: 1.		
286	HSYBL15	793624	603	117 - 284	1216				AR061: 1, AR089: 0 S0212: 1, H0551: 1 and L0366: 1.		
287	HTEKH29	1104299	296	2 - 931	909	Pro-26 to Gly-32, Ala-133 to Cys-138, Asp-145 to Lys-152, Leu-164 to Ser-173, Lys-178 to Ser-183, Asp-260 to Phe-266.					
		660053	604	2 - 286	1217	Pro-26 to Gly-32.					
		855660	297	478 - 2028	910	Ser-27 to Glu-35, Thr-43 to Phe-52, Val-59 to Gln-70, His-74 to Val-79.			AR089: 8, AR061: 7		

							Pro-108 to Lys-122, Ala-130 to Phe-141, Val-145 to Ala-151, Asp-159 to Glu-165, Ser-185 to Lys-191.					
288	HTGEL46	1151520	298	331 - 705	911		Glu-55 to His-72.		AR089: 0, AR061: 0 S0218: 1, H0264: 1 and S0053: 1.			
		685425	605	323 - 457	1218							
289	HTGFA05	1198110	299	3 - 1262	912		Ile-45 to Arg-52, Phe-77 to Pro-85, Leu-111 to Val-118, Ile-124 to Thr-129, Pro-139 to Gly-151, Arg-186 to Gly-215, Lys-223 to Glu-230.		AR061: 1, AR089: 0 H0556: 10, L0748: 8, H0620: 7, L0747: 7, L0637: 5, H0265: 4, H0013: 4, H0551: 4, L0776: 4, L0663: 4, L0596: 4, H0622: 3, H0617: 3, L0772: 3, L0766: 3, S0126: 3, L0751: 3, L0752: 3, S0031: 3, L0593: 3, H0657: 2, S0360: 2, S0222: 2, T0115: 2, H0009: 2, L0471: 2, H0594: 2, H0288: 2, H0039: 2, H0424: 2, H0135: 2, H0040: 2,			

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290	HTLDU61	1165319	300	690 - 220	913	Cys-59 to Thr-68, Ile-78 to Thr-83, Pro-93 to Gly-105, Arg-140 to Gly-169, Lys-177 to Glu-184.	AR061: 2, AR089: 2 H0253: 1, S0010: 1, L0456: 1, H0695: 1 and L0657: 1.		
		530316	607	63 - 224	1220	Gln-5 to His-17, Pro-30 to Ser-40, Pro-42 to Thr-65, Gly-102 to Gln-107, Ala-112 to Lys-118, Ser-127 to Thr-138.			
291	HTOFT34	1152490	301	361 - 609	914		AR089: 8, AR061: 5 H0264: 2 and L0367: 1.		
		527144	608	106 - 270	1221				
292	HTTDH46	1152491	302	2 - 1144	915	Gly-50 to Asp-59, Thr-220 to Phe-233, Glu-285 to Tyr-291, Thr-298 to Arg-303, Ala-353 to Asn-358.	AR061: 7, AR089: 2 H0253: 10, H0617: 8, H0559: 7, H0265: 6, H0618: 5, H0551: 5, H0052: 4, H0620: 4, L0794: 4, H0556: 3, H0135: 3, H0087: 3, L0659: 3, L0666: 3, L0663: 3, L0438: 3, H0522: 3, L0749: 3,		

[illegible]

	H0581: 1, H0194: 1, H0327: 1, H0046: 1, H0009: 1, H0178: 1, H0012: 1, H0023: 1, H0201: 1, S0051: 1, H0083: 1, S6028: 1, H0266: 1, H0271: 1, H0428: 1, H0604: 1, H0417: 1, H0181: 1, H0163: 1, H0038: 1, H0634: 1, H0063: 1, H0264: 1, H0412: 1, S0038: 1, L0351: 1, H0359: 1, S0150: 1, H0646: 1, H0538: 1, S0002: 1, S0426: 1, L0640: 1, L0772: 1, L0372: 1, L0641: 1, L0643: 1, L0764: 1, L0767: 1, L0768: 1, L0766: 1, L0375: 1, L0378: 1, L0806: 1, L0652: 1, L0656: 1, L0636: 1, L0790: 1, L0664: 1, H0144: 1, S0374: 1, H0520: 1,					
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293	HTTIO05	951114	609	3 - 500	1222	Arg-1 to Thr-15.	H0547: 1, H0593: 1, H0682: 1, H0651: 1, S0328: 1, H0539: 1, S0380: 1, S0332: 1, S3014: 1, S0027: 1, L0754: 1, L0750: 1, L0755: 1, L0757: 1, L0758: 1, S0031: 1, L0593: 1, H0667: 1, H0217: 1, H0423: 1, H0422: 1 and S0042: 1.		
		1229905	303	1367 - 1624	916		AR061: 57, AR089: 49 L0770: 2, S0114: 1, L0717: 1, H0634: 1, L0773: 1, L0521: 1, L0803: 1, L0791: 1, L0664: 1, S0330: 1, S0380: 1, L0759: 1 and H0653: 1.		
294	HWHGY45	931037	610	1286 - 1564	1223				
		911621	304	3 - 203	917		AR089: 23, AR061: 3 S0144: 2, H0662: 1, H0586: 1, H0587: 1, T0060: 1, H0696: 1 and L0745: 1.		

295	HWLQR48	1128304	305	338 - 508	918		AR089: 23, AR061: 6 L0518: 4, L0731: 3, L0637: 2, H0659: 2, H0170: 1, S6024: 1, S0360: 1, H0586: 1, H0050: 1, L0598: 1, L0763: 1, L0666: 1, L0663: 1, L0743: 1, L0745: 1 and L0601: 1.		
296	HWLQX76	914556	611	338 - 475	1224		Gly-1 to Pro-6, His-18 to Ser-23, Asn-45 to Thr-56, Ala-65 to Arg-70, Asp-84 to Ile-89, Glu-109 to Leu-114, Lys-146 to Lys-155. His-12 to Ser-17, Asn-39 to Thr-50, Ala-59 to Arg-64, Asp-78 to Ile-83.	AR089: 1, AR061: 1 H0553: 3, S0360: 1, H0561: 1, L0526: 1, H0519: 1, S0126: 1, H0543: 1 and L0697: 1.	
		1152280	306	2 - 466	919				
		894607	612	1 - 996	1225				
297	HATDD09	1165331	307	428 - 1027	920		AR061: 4, AR089: 4 L0361: 2, H0662: 1, T0039: 1, H0156: 1, H0052: 1, H0194: 1, H0179: 1, H0135: 1,		

									L0662: 1, L0364: 1, L0790: 1, L0666: 1, S0028: 1 and S0194: 1.		
298	HBJGT03	573794	613	2 - 184	1226				AR061: 5, AR089: 3 L0769: 2, H0318: 1 and L0787: 1.		
		1105484	308	352 - 89	921			Ser-33 to Ala-47.			
		923800	614	35 - 226	1227			Ala-16 to Ser-22, Pro-31 to Leu-38, Ser-41 to Gly-48.			
299	HMTMF45	1141737	309	33 - 401	922				AR061: 1, AR089: 1 L0766: 3, L0777: 2, S0116: 1, S0376: 1, H0457: 1, L0771: 1, L0803: 1, L0804: 1, L0657: 1, L0659: 1, H0525: 1 and L0750: 1.		
		553382	615	2 - 376	1228			Arg-3 to Asp-14, Glu-53 to Gly-59, Asp-105 to Asn-113.			
300	HHPDV86	522953	310	1 - 636	923			Thr-6 to Asp-14, Ser-36 to Glu-41, Ala-159 to Trp-168, Ser-176 to Lys-181.	AR061: 7, AR089: 3 L0809: 3, L0747: 3, S0360: 2, H0422: 2, H0556: 1, S0040: 1, H0664: 1, S0358: 1, T0048: 1, H0051: 1,		

301	HE8BT56	732602	311	45 - 377	924			L0794: 1, L0791: 1, L0664: 1, S0052: 1, S0053: 1, H0701: 1, H0689: 1, H0690: 1, H0521: 1, H0626: 1 and L0595: 1.		
								AR061: 3, AR089: 2 L0766: 7, L0439: 3, L0749: 3, H0013: 2, L0776: 2, L0740: 2, L0746: 2, H0083: 1, H0366: 1, S0422: 1, L0787: 1, L0791: 1, L0779: 1, L0780: 1 and L0752: 1.		
302	HUJDH06	907613	312	304 - 672	925	Pro-10 to Lys-22.		AR089: 1, AR061: 1 H0650: 1, H0591: 1 and S0390: 1.		
303	HOEJG61	907614	313	174 - 671	926	Lys-31 to Ser-37, Leu-112 to Ser-119.		AR061: 7, AR089: 2 L0769: 3, L0766: 2, L0638: 1, S0126: 1, H0683: 1, L0745: 1 and H0506: 1.		
304	HE8PN24	907620	314	2 - 724	927	Gly-59 to Glu-66, Cys-87 to Asn-93, Asn-122 to Trp-127,		AR061: 2, AR089: 0 H0013: 2, S0142: 2, L0740: 1 and L0747: 1.		

305	HGBHI37	909745	315	2 - 451	928	Arg-129 to Ser-134, Ala-144 to Asp-149, Asn-176 to Ala-182.	AR089: 1, AR061: 1 H0656: 1 and H0014: 1.			
306	HCHOK82	909755	316	1 - 1089	929	Leu-52 to Leu-66, Trp-97 to Leu-103.	AR089: 4, AR061: 3 H0457: 3, H0271: 3, H0543: 3, H0422: 2, H0583: 1, H0650: 1, H0484: 1, H0483: 1, S0442: 1, H0580: 1, S0140: 1, H0486: 1, H0250: 1, H0050: 1, H0630: 1, H0264: 1, H0488: 1, H0487: 1, S0002: 1, L0439: 1, H0707: 1, H0136: 1 and H0677: 1.			
307	HFPCH24	912608	317	2 - 352	930	Thr-5 to Asn-13, Pro-69 to Ala-76.	AR061: 3, AR089: 3 L0803: 3, S0222: 1, L0021: 1, H0510: 1, L0774: 1, L0777: 1, L0731: 1, S0260: 1 and S0434: 1.			
308	HTTKF86	912689	318	2 - 223	931	Arg-9 to Pro-16.	AR061: 4, AR089: 3	22q13.1		103050,

								H0634: 1 and H0522: 1.		103050, 124030, 124030, 138981, 182380, 188826, 190040, 190040, 190040
309	HCESA79	912709	319	25 - 315	932	Glu-42 to Arg-55, Lys-63 to Gly-68.	AR061: 6, AR089: 2 H0194: 2, L0748: 2, H0052: 1, T0010: 1, H0658: 1, S0380: 1 and L0366: 1.	16p13.3		141750, 141800, 141800, 141800, 141800, 141850, 141850, 141850, 141850, 156850, 186580, 191092, 600140, 600273, 601313, 601785

310	HDTBJ28	912714	320	533 - 243	933		AR089: 38, AR061: 25 H0393: 1 and H0486: 1.		
311	HDPBF48	912783	321	3 - 809	934	Asp-52 to Thr-62, Thr-101 to Trp-112, Gly-131 to Asn-141, Asp-173 to Ile-179.	AR089: 8, AR061: 3 L0758: 4, H0521: 3, L0163: 2, L0783: 2, L0749: 2, S0342: 1, L0021: 1, H0318: 1, H0373: 1, H0083: 1, H0674: 1, H0494: 1, H0529: 1, L0768: 1, L0790: 1, H0519: 1, S0126: 1, H0670: 1, L0602: 1, L0748: 1, L0777: 1, L0752: 1, L0759: 1, L0588: 1, H0542: 1 and H0422: 1.		
312	HTPFY55	912928	322	117 - 563	935	Val-14 to Val-19, Ser-27 to Ser-32.	AR089: 3, AR061: 2 H0039: 1, H0622: 1 and H0644: 1.		
313	HMSCM47	923632	323	2 - 685	936	Gln-13 to Lys-19, Gln-59 to Tyr-69, Asp-116 to His-126, Gly-164 to Lys-170, Gln-182 to Gly-187, Tyr-207 to Gly-212.	AR089: 6, AR061: 3 H0521: 3, L0794: 2, L0805: 2, H0520: 2, L0602: 2, L0756: 2, H0170: 1, H0556: 1, S0134: 1, S0116: 1,		

					H0341: 1, H0662: 1, S0354: 1, S0360: 1, H0580: 1, H0619: 1, S0278: 1, H0574: 1, H0599: 1, H0590: 1, H0596: 1, L0471: 1, H0024: 1, H0014: 1, L0163: 1, H0051: 1, H0510: 1, H0615: 1, H0644: 1, H0617: 1, H0068: 1, L0060: 1, H0551: 1, S0450: 1, S0002: 1, L0369: 1, L0763: 1, L0371: 1, L0631: 1, L0637: 1, L0800: 1, L0764: 1, L0363: 1, L0767: 1, L0549: 1, L0803: 1, L0774: 1, L0776: 1, L0809: 1, L0791: 1, H0144: 1, H0658: 1, H0522: 1, H0478: 1, S3014: 1, S0028: 1, L0747: 1, L0749: 1, L0752: 1, L0753: 1, L0731: 1, L0758: 1,				
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314	HEOQA56	925132	324	234 - 1	937	Arg-5 to His-10, Ser-40 to Gln-48.	L0759: 1, L0601: 1, L0366: 1 and H0506: 1. AR089: 2, AR061: 2 H0521: 8, H0457: 6, H0494: 4, L0439: 4, S0152: 3, S0206: 3, H0013: 2, H0551: 2, H0623: 2, L0789: 2, L0438: 2, S0027: 2, L0601: 2, H0556: 1, S0040: 1, H0675: 1, H0645: 1, H0393: 1, H0411: 1, H0549: 1, H0592: 1, H0250: 1, H0575: 1, H0581: 1, H0266: 1, H0628: 1, H0598: 1, H0038: 1, H0413: 1, H0056: 1, H0561: 1, S0150: 1, H0633: 1, H0647: 1, S0426: 1, H0529: 1, L0369: 1, L0766: 1, L0806: 1, H0703: 1, H0519: 1, H0522: 1, S0028: 1, L0740: 1, L0750: 1, S0031: 1,		
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315	HTPCQ24	925349	325	1 - 450	938	Gly-1 to Leu-26, Thr-28 to Leu-35.	L0595: 1 and S0011: 1. AR061: 2, AR089: 1 H0046: 21, L0747: 10, H0039: 3, H0024: 2, L0766: 2, L0654: 2, L0748: 2, L0439: 2, L0779: 2, L0777: 2, T0049: 1, S0212: 1, H0662: 1, S0354: 1, S0045: 1, H0393: 1, H0107: 1, H0266: 1, S0250: 1, H0615: 1, H0688: 1, H0040: 1, H0616: 1, H0551: 1, H0641: 1, L0770: 1, L0637: 1, L0764: 1, L0767: 1, L0768: 1, L0659: 1, L0647: 1, L0666: 1, S0027: 1, S0028: 1, L0743: 1, L0749: 1, L0750: 1, L0780: 1, L0755: 1, L0758: 1 and L0759: 1.		
316	HWAEI37	929481	326	2 - 415	939		AR089: 5, AR061: 1 H0581: 1 and H0519: 1.		

317	HDPSF03	969536	327	1 - 1269	940		AR089: 9, AR061: 3		
318	HLHST63	581528	328	28 - 423	941	Ala-1 to Gly-15, Arg-32 to Ser-38, Thr-62 to His-68, Ser-104 to Thr-110, Gly-117 to Thr-122.	L0731: 28, L0740: 22, L0747: 21, L0748: 20, S0003: 18, L0754: 17, L0438: 12, L0439: 12, L0775: 11, L0752: 11, S0026: 11, L0770: 10, H0521: 10, L0749: 9, S0358: 8, L0766: 8, L0659: 8, L0591: 8, S0192: 8, S0360: 7, L0764: 7, H0522: 7, S0010: 6, H0039: 6, S0002: 6, L0666: 6, L0665: 6, H0144: 6, S0126: 6, L0750: 6, L0755: 6, L0758: 6, S0426: 5, L0662: 5, L0663: 5, L0759: 5, L0599: 5, T0049: 4, S0282: 4, H0402: 4, S0354: 4, H0619: 4, H0620: 4, H0266: 4, H0032: 4, H0641: 4, S0422: 4, L0771: 4,		

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	S0116: 1, H0341: 1, H0661: 1, H0177: 1, H0306: 1, S0418: 1, S0356: 1, H0208: 1, S0046: 1, H0645: 1, H0393: 1, S0300: 1, L0717: 1, S6014: 1, H0438: 1, H0586: 1, H0333: 1, H0331: 1, H0632: 1, L0622: 1, H0486: 1, T0040: 1, L0586: 1, T0060: 1, H0244: 1, H0599: 1, H0098: 1, H0590: 1, H0004: 1, H0581: 1, H0421: 1, S0049: 1, H0196: 1, L2250: 1, H0235: 1, H0596: 1, T0115: 1, T0110: 1, H0597: 1, H0546: 1, H0545: 1, H0150: 1, H0009: 1, H0178: 1, H0123: 1, L0471: 1, H0012: 1, H0014: 1, H0015: 1, H0373: 1, S0388: 1, T0010: 1,	
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H0239: 1, H0510: 1, H0594: 1, S6028: 1, H0267: 1, H0179: 1, H0188: 1, H0028: 1, H0252: 1, H0615: 1, H0092: 1, T0006: 1, H0030: 1, L0142: 1, H0628: 1, H0617: 1, L0055: 1, H0383: 1, H0674: 1, H0400: 1, H0135: 1, H0163: 1, H0591: 1, H0038: 1, H0040: 1, H0551: 1, H0488: 1, H0412: 1, H0059: 1, H0100: 1, H0429: 1, H0561: 1, S0440: 1, H0509: 1, S0150: 1, H0647: 1, S0344: 1, S0210: 1, L0763: 1, L0638: 1, L0639: 1, L0637: 1, L0772: 1, L0646: 1, L0768: 1, L0794: 1, L0803: 1, L0804: 1, L0378: 1, L0652: 1, L0653: 1, L0655: 1,						
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319	HFAAJ44	646715	616	151 - 20	1229	Cys-11 to His-18.	L0606: 1, L0657: 1, L0493: 1, L0518: 1, L0782: 1, L0545: 1, L0529: 1, L0647: 1, L0792: 1, L0532: 1, S0148: 1, H0547: 1, H0593: 1, H0365: 1, H0689: 1, H0682: 1, H0684: 1, H0435: 1, H0670: 1, H0666: 1, S0380: 1, L0602: 1, S0152: 1, S0013: 1, S0146: 1, H0555: 1, H0478: 1, H0540: 1, S3012: 1, S0037: 1, S0206: 1, L0756: 1, L0777: 1, H0444: 1, H0595: 1, L0589: 1, S0011: 1, H0668: 1, H0665: 1, H0667: 1, S0194: 1, S0276: 1, H0542: 1, S0384: 1, H0506: 1 and H0352: 1.		
		744764	617	39 - 221	1230				
		489201	329	3 - 299	942				

322	HFTAR20	670041	332	3 - 443	945		AR089: 6, AR061: 4 L0749: 6, L0794: 4, H0123: 1, L0768: 1 and S0194: 1.		
323	HCUFD32	699379	333	1 - 498	946	Thr-1 to Leu-11, Lys-24 to Ile-29, Gln-134 to Asn-144, Gln-150 to Thr-165.	AR089: 7, AR061: 3 L0754: 6, L0439: 2, L0751: 2, L0747: 2, H0661: 1, H0402: 1, H0272: 1, L0438: 1, H0696: 1 and L0779: 1.		
324	HKAEO39	705332	334	2 - 463	947	Lys-20 to Ser-28, Arg-44 to Ala-52, Leu-83 to Glu-89.	AR089: 0, AR061: 0 L0792: 2, S0420: 1, H0645: 1, H0494: 1, L0806: 1, L0807: 1, L0740: 1 and L0752: 1.		
325	HLWBR95	734474	335	3 - 476	948		AR089: 3, AR061: 1 S0420: 1, H0550: 1, H0587: 1, H0485: 1, H0150: 1, H0553: 1, T0042: 1, L0530: 1 and S0152: 1.	10q23 174900, 236730, 601493	
326	HPWCJ63	772553	336	148 - 807	949	Lys-213 to Gly-220.	AR054: 2, AR051: 1, AR061: 0, AR089: 0, AR050: 0 S0001: 1, H0191: 1 and S0044: 1.		

		957495	618	1239 - 580	1231	Lys-213 to Gly-220.			
327	HBXCM35	782911	337	592 - 98	950		AR089: 8, AR061: 4 L0743: 2, S0040: 1, H0663: 1, H0427: 1, H0545: 1, S0250: 1, H0087: 1, S0038: 1, L0804: 1 and L0783: 1.		
328	HULBN83	857836	338	1 - 636	951		AR089: 1, AR061: 1 H0619: 2, L0779: 2, S0222: 1, H0530: 1, H0433: 1, L0766: 1 and L0753: 1.		
329	HAGET77	885265	339	86 - 850	952	Lys-26 to Gln-36, Leu-50 to Glu-56, Gly-93 to Thr-106, Gln-108 to Gly-122, Gly-132 to Gln-138, Ser-144 to Trp-153, Glu-155 to Glu-171, Lys-178 to Pro-198, Val-207 to Asn-230, Arg-235 to Asp-247.	AR061: 4, AR089: 2 S0010: 3, S0036: 3, L0766: 3, S0222: 2, S0346: 2, H0310: 2, H0327: 2, H0457: 2, H0656: 1, S0282: 1, S6016: 1, S0665: 1, L2250: 1, H0051: 1, S0386: 1, H0342: 1, S0031: 1, L0366: 1 and H0543: 1.		
330	HMSOZ55	910911	340	3 - 503	953	Lys-22 to Gly-27.	AR089: 6, AR061: 3 S0282: 1, T0040: 1, H0013: 1, S0182: 1,		

331	HAPOR42	911292	341	6 - 701	954			S0426: 1, H0670: 1, H0667: 1 and H0542: 1.		
332	HMVAU10	911449	342	2 - 538	955			AR089: 21, AR061: 10 H0156: 1, H0575: 1, H0590: 1, H0263: 1 and L0362: 1.		
333	HTTFY29	911454	343	3 - 644	956		Arg-37 to Arg-44, Asn-47 to Glu-56, Lys-65 to Glu-70, Arg-78 to Pro-83, Gln-98 to Asp-106, Pro-142 to Ile-151, Ala-154 to Thr-180.	AR054: 16, AR051: 13, AR061: 8, AR089: 3, AR050: 1 H0040: 1, H0022: 1, S0152: 1 and H0521: 1.		
334	HHFJY06	911456	344	81 - 584	957		Glu-11 to Ser-21, Asn-52 to Ser-57, Arg-81 to Met-88, Glu-139 to Tyr-146, Glu-153 to Leu-159.	AR089: 10, AR061: 6 H0619: 1, S0036: 1, H0135: 1 and H0520: 1.		
335	HPCIK72	911459	345	283 - 2	958			AR089: 1, AR061: 0 S0358: 1, H0642: 1 and H0264: 1.		
336	HFIDT84	919878	346	64 - 2151	959		Asp-51 to His-60, Thr-105 to Pro-117, Asp-143 to Ala-151,	AR089: 9, AR061: 5 S0192: 2, S0222: 1, H0562: 1, H0373: 1 and		

							Asp-167 to Ile-192, Ala-212 to Thr-223, Arg-325 to Asp-346, Lys-354 to Glu-359, Gln-390 to Asp-395, Arg-406 to Ser-412, Gln-431 to Asp-438, Ser-447 to Leu-465, Arg-516 to Thr-522, Lys-561 to Ser-570, Pro-583 to Pro-589, Tyr-625 to Asn-631, Pro-644 to Arg-650.	S0242: 1.			
337	HMCAY88	924874	347	40 - 516	960	Glu-19 to Asp-28, Tyr-37 to Ala-42, Pro-53 to Leu-59, Ile-67 to Gly-74, Arg-152 to Val-158.	AR089: 11, AR061: 6 L0748: 10, L0751: 9, L0769: 7, L0779: 7, S0126: 5, S0022: 4, L0775: 4, L0740: 4, L0747: 4, L0752: 4, L0731: 4, L0596: 4, S0142: 3, L0771: 3, L0757: 3, L0599: 3, T0039: 2, H0013: 2, S0346: 2, S0003: 2, T0041: 2, S0344: 2, L0770: 2, L0773: 2,				

					L0766: 2, L0776: 2, L0663: 2, L0565: 2, S0027: 2, L0742: 2, L0754: 2, L0750: 2, L0753: 2, L0759: 2, L0588: 2, L0362: 2, H0624: 1, L0002: 1, H0656: 1, S0212: 1, S0420: 1, S0356: 1, H0441: 1, L0034: 1, L0738: 1, H0546: 1, H0012: 1, H0620: 1, H0024: 1, H0014: 1, H0083: 1, H0622: 1, T0006: 1, H0617: 1, H0068: 1, H0090: 1, H0063: 1, H0334: 1, H0561: 1, S0150: 1, H0633: 1, L0372: 1, L0662: 1, L0804: 1, L0774: 1, L0656: 1, L0636: 1, L0635: 1, L0783: 1, L0384: 1, L0809: 1, L0528: 1, L0666: 1, L0664: 1, H0144: 1, H0547: 1,				
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338	HKAIP73	928809	348	1455 - 487	961	Ser-3 to Asp-8, Ser-39 to Pro-61, Ser-63 to Ser-69, > Lys-144 to Thr-150, Asp-187 to Gly-193.	AR089: 3, AR061: 2 H0031: 9, L0659: 7, S0358: 5, H0622: 5, H0494: 5, L0438: 4, L0743: 4, S0132: 3, H0040: 3, L0800: 3, L0771: 3, S0354: 2, H0014: 2, L0483: 2, L0764: 2, L0783: 2, L0587: 2, L0601: 2, S0114: 1, H0661: 1, S0356: 1, S0442: 1, S0360: 1, H0592: 1, H0587: 1, H0036: 1, H0590: 1, H0024: 1, H0510: 1, H0252: 1, H0039: 1, H0553: 1, S0440: 1, L0772: 1,	H0670: 1, H0648: 1, H0539: 1, S0152: 1, S0406: 1, H0540: 1, S3014: 1, L0745: 1, L0777: 1, L0755: 1, L0758: 1, H0445: 1, L0592: 1, H0667: 1, S0194: 1 and H0423: 1.		
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339	HFVHV40	945849	349	6 - 680	962	Pro-8 to Arg-29, Tyr-156 to Asp-161, Glu-172 to Pro-184, Arg-194 to Asn-203.	L0646: 1, L0374: 1, L0773: 1, L0766: 1, L0803: 1, L0804: 1, L0774: 1, L0784: 1, L0806: 1, L0653: 1, L0655: 1, S0374: 1, S0328: 1, S3012: 1, L0749: 1, L0731: 1, L0758: 1 and H0677: 1.			
340	HTJN180	952231	350	2 - 598	963		AR061: 5, AR089: 3 S0152: 3, H0619: 2, S6024: 1, H0341: 1, S0212: 1, H0393: 1, H0592: 1, H0575: 1, H0036: 1, H0052: 1, N0006: 1, H0083: 1, L0483: 1, H0100: 1, H0494: 1, S0144: 1, S0002: 1, H0703: 1, H0522: 1, H0134: 1, H0436: 1 and H0653: 1. AR089: 10, AR061: 4 H0650: 2, S3014: 2, H0265: 1, H0581: 1, L0034: 1, H0488: 1, H0547: 1, H0518: 1.			

341	HEAAE08	959970	351	133 - 621	964	Pro-1 to Pro-12, Pro-53 to Gly-58, Gly-65 to Ser-71, Gly-106 to Lys-111, Lys-143 to Gly-163.	AR061: 10, AR089: 4 L0789: 6, L0809: 2, H0669: 1, H0369: 1, H0252: 1, L0055: 1, L0763: 1, L0770: 1, L0638: 1, L0803: 1, L0805: 1, L0776: 1, L0753: 1, L0758: 1, L0592: 1 and H0543: 1.	S0152: 1, S0260: 1 and L0366: 1.		
342	HDPLU91	963199	352	2 - 748	965	Pro-53 to Val-58, Pro-85 to Ser-95, Gln-132 to Gly-138.	AR089: 16, AR061: 5 L0439: 10, L0526: 6, L0005: 5, L0740: 5, S0422: 4, L0438: 4, L0758: 4, L0581: 4, H0370: 3, H0486: 3, S0003: 3, H0144: 3, H0659: 3, H0672: 3, L0744: 3, L0754: 3, L0731: 3, L0595: 3, H0657: 2, H0664: 2, S0418: 2, S0376: 2, H0431: 2, H0050: 2, L0471: 2, H0083: 2, H0266: 2, H0090: 2,			

					H0616: 2, L0770: 2, L0769: 2, L0761: 2, L0766: 2, L0655: 2, L0657: 2, L0659: 2, L0783: 2, L0519: 2, L0666: 2, L0756: 2, L0759: 2, S0260: 2, H0595: 2, L0588: 2, L0589: 2, L0590: 2, L0608: 2, S0192: 2, H0265: 1, T0049: 1, H0650: 1, L0481: 1, H0638: 1, S0356: 1, T0008: 1, H0208: 1, S0045: 1, L0010: 1, H0611: 1, H0455: 1, H0574: 1, H0492: 1, H0635: 1, L0021: 1, H0575: 1, S0010: 1, H0318: 1, H0581: 1, H0052: 1, H0251: 1, H0597: 1, H0046: 1, L0157: 1, H0051: 1, S0048: 1, H0188: 1, L0483: 1, H0644: 1, L0455: 1, S0036: 1,				
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343	HAPRM21	963200	353	1 - 630	966	Gln-8 to Gly-14, Thr-164 to Gly-183, Pro-197 to Asp-210.	AR089: 25, AR061: 5 H0123: 2, L0754: 2, H0650: 1, H0550: 1,	AR089: 25, AR061: 5 H0123: 2, L0754: 2, H0650: 1, H0550: 1,	
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344	HTDAB30	965320	354	3 - 944	967				H0244: 1, H0427: 1, H0575: 1, S0010: 1 and L0698: 1.		
									AR089: 5, AR061: 4 S0152: 7, L0748: 7, L0779: 6, L0766: 5, H0591: 4, L0771: 4, L0749: 4, L0777: 4, L0759: 4, H0556: 3, L0803: 3, L0783: 3, H0521: 3, L0754: 3, L0731: 3, L0595: 3, H0423: 3, H0170: 2, H0657: 2, H0341: 2, H0013: 2, H0598: 2, H0412: 2, H0494: 2, L0768: 2, L0526: 2, L0663: 2, S0328: 2, L0755: 2, L0757: 2, H0542: 2, S0420: 1, S0358: 1, S0408: 1, H0619: 1, H0587: 1, H0486: 1, T0060: 1, H0575: 1, H0036: 1, H0318: 1, H0581: 1, H0434: 1, H0544: 1,		

								H0014: 1, H0687: 1, H0644: 1, H0163: 1, H0090: 1, H0551: 1, H0477: 1, H0264: 1, H0268: 1, H0623: 1, H0560: 1, S0370: 1, S0002: 1, H0529: 1, L0520: 1, L0769: 1, L0774: 1, L0606: 1, L0807: 1, L0659: 1, L0384: 1, L0790: 1, L0664: 1, S0052: 1, H0702: 1, H0547: 1, H0519: 1, H0684: 1, H0518: 1, H0696: 1, S0432: 1, L0780: 1, L0752: 1, L0758: 1, L0596: 1, L0608: 1, H0667: 1, H0543: 1 and S0446: 1.					
345	H2CBN90	966919	355	3 - 821	968			AR061: 4, AR089: 4 L0794: 6, S0360: 3, T0110: 2, L0455: 2, L0649: 2, L0498: 2, L0659: 2, L0791: 2, L0748: 2, L0731: 2,					

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						H0485: 1, L0105: 1, L0738: 1, H0545: 1, H0633: 1, L0646: 1, L0662: 1, L0768: 1, L0803: 1, L0774: 1, L0806: 1, L0790: 1, H0144: 1, H0690: 1, H0435: 1, S0032: 1, L0740: 1, L0747: 1, L0779: 1 and L0758: 1.			
346	HETFJ47	971305	356	3 - 1328	969	AR061: 2, AR089: 1 L0596: 7, H0622: 5, L0747: 5, H0046: 4, L0372: 4, L0764: 3, L0662: 3, L0657: 3, L0783: 3, L0663: 3, L0752: 3, H0662: 2, S0356: 2, H0040: 2, H0538: 2, L0646: 2, L0771: 2, L0774: 2, L0805: 2, L0809: 2, L0666: 2, L0665: 2, H0435: 2, L0751: 2, L0777: 2, L0608: 2, H0624: 1, H0686: 1, H0295: 1, H0241: 1,			

347	HADEX52	971351	357	38 - 1354	970	Arg-11 to Arg-18, Glu-23 to Glu-28, Asn-40 to Leu-45, Thr-53 to Asp-58, Lys-74 to Asp-82, Val-92 to Glu-97,	S0418: 1, S0358: 1, S0376: 1, S0360: 1, S0132: 1, H0642: 1, H0590: 1, H0150: 1, H0620: 1, H0023: 1, H0356: 1, H0424: 1, H0213: 1, H0617: 1, H0169: 1, H0634: 1, H0063: 1, T0067: 1, H0488: 1, H0334: 1, S0370: 1, H0652: 1, L0645: 1, L0773: 1, L0648: 1, L0806: 1, L0776: 1, L0541: 1, L0789: 1, L0790: 1, L0664: 1, S0374: 1, H0689: 1, H0666: 1, H0672: 1, H0478: 1, L0748: 1, L0779: 1, S0436: 1 and H0506: 1.		
347	HADEX52	971351	357	38 - 1354	970	Arg-11 to Arg-18, Glu-23 to Glu-28, Asn-40 to Leu-45, Thr-53 to Asp-58, Lys-74 to Asp-82, Val-92 to Glu-97,	AR054: 40, AR050: 30, AR051: 28, AR089: 1, AR061: 1 S0270: 8, S0268: 7, L0731: 4, L0471: 3, H0201: 2, H0547: 2,		

						Ser-104 to Asn-109, Asp-127 to Phe-133, Gln-158 to Asp-170, Asn-177 to Ala-207.	S0274: 2, L0754: 2, L0604: 2, S0202: 1, S0252: 1, S0360: 1, H0550: 1, H0600: 1, H0333: 1, H0486: 1, H0013: 1, H0427: 1, H0599: 1, H0575: 1, S0010: 1, H0194: 1, H0327: 1, H0569: 1, H0594: 1, S0628: 1, S0250: 1, H0622: 1, L0544: 1, H0144: 1, L0438: 1, H0519: 1, S0126: 1, L0744: 1, L0747: 1, L0777: 1, S0242: 1 and S0196: 1.		
348	HTADZ74	811489	358	23 - 586	971	Ile-5 to Lys-10, Arg-78 to Asp-92.	AR050: 18, AR089: 2, AR061: 2, AR051: 2, AR054: 1, S0114: 1, H0069: 1, H0014: 1, L0667: 1, L0804: 1, L0659: 1, S0052: 1 and H0422: 1.		
349	HAPNZ77	887072	359	1 - 483	972	Lys-82 to Gln-87, Asp-103 to Ala-108, Glu-122 to Lys-127.	AR089: 70, AR061: 14, AR050: 9, AR051: 1, AR054: 1		

350	HELDR74	963001	360	3 - 1223	973	His-14 to Gln-19.	L0766: 2, H0575: 1, H0264: 1, L0761: 1 and L0804: 1.		
							AR089: 1, AR061: 0 H0305: 4, L0731: 3, L0581: 3, H0622: 2, H0059: 2, L0764: 2, L0766: 2, L0741: 2, L0740: 2, L0749: 2, H0423: 2, H0149: 1, H0159: 1, S0114: 1, H0656: 1, H0255: 1, H0306: 1, H0402: 1, S0045: 1, H0351: 1, H0550: 1, H0441: 1, H0036: 1, T0048: 1, H0318: 1, H0581: 1, H0024: 1, H0051: 1, H0083: 1, H0510: 1, H0617: 1, H0412: 1, H0280: 1, H0647: 1, L0646: 1, L0374: 1, L0385: 1, L0662: 1, L0767: 1, L0794: 1, L0649: 1, L0774: 1, L0806: 1, L0653: 1,		

351	HDPLJ22	859915	361	2 - 547	974	Phe-20 to Lys-37, Asn-108 to Arg-116.	AR089: 1, AR061: 0 L0591: 20, L0748: 13, H0090: 5, H0521: 4, L0758: 4, H0556: 3, H0656: 3, S0358: 3, H0038: 3, S0002: 3, L0794: 3, L0766: 3, L0803: 3, L0805: 3, L0791: 3, L0665: 3, H0547: 3, S0328: 3, L0747: 3, H0423: 3, H0624: 2, S0420: 2, S0046: 2, H0427: 2, H0156: 2, H0046: 2, L0471: 2, H0510: 2, H0424: 2, H0181: 2, H0264: 2, H0100: 2, S0426: 2, L0631: 2,			L0657: 1, L0659: 1, L0783: 1, S0126: 1, H0690: 1, H0670: 1, H0672: 1, S0328: 1, S0380: 1, H0555: 1, L0748: 1, L0752: 1, L0758: 1, S0194: 1, H0542: 1 and H0422: 1.		
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	H0539: 2, S0380: 2, S0152: 2, H0555: 2, S3014: 2, S0206: 2, L0777: 2, L0731: 2, H0422: 2, H0686: 1, L0002: 1, H0657: 1, H0663: 1, H0662: 1, S0348: 1, S0360: 1, S0007: 1, S0278: 1, H0600: 1, H0497: 1, H0559: 1, T0039: 1, H0013: 1, H0599: 1, H0575: 1, H0004: 1, H0318: 1, H0581: 1, H0421: 1, H0263: 1, H0050: 1, H0082: 1, H0373: 1, H0071: 1, H0629: 1, S0003: 1, H0328: 1, H0031: 1, H0553: 1, H0111: 1, H0628: 1, H0617: 1, H0673: 1, S0364: 1, H0135: 1, H0163: 1, T0067: 1, H0561: 1, S0440: 1, S0344: 1, L0761: 1, L0764: 1,						
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352	HPMLD11	890204	362	562 - 2	975	Gln-11 to Trp-22, Arg-27 to Gly-32, Pro-47 to Gly-53.	AR054: 115, AR050: 108, AR051: 87, AR061: 4, AR089: 2 H0644: 3, S0408: 1, S0280: 1, H0620: 1, S0364: 1, L0637: 1, L0764: 1, S0044: 1, L0611: 1, L0777: 1, L0755: 1, L0731: 1 and S0194: 1.		
							L0771: 1, L0773: 1, L0650: 1, L0776: 1, L0655: 1, L0606: 1, L0629: 1, L0659: 1, L0809: 1, L0792: 1, L0666: 1, H0520: 1, H0593: 1, H0689: 1, H0659: 1, S0330: 1, H0522: 1, H0627: 1, L0742: 1, L0439: 1, L0740: 1, L0749: 1, L0779: 1, L0752: 1, L0757: 1, L0759: 1, H0445: 1, L0485: 1, H0653: 1, S0196: 1, H0542: 1 and H0506: 1.		

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353	HMVDZ78	938574	363	2 - 250	976	AR089: 2, AR061: 2 L0659: 8, L0666: 8, L0751: 7, L0665: 6, L0528: 5, L0743: 5, L0663: 4, H0052: 3, L0638: 3, L0646: 3, L0764: 3, L0662: 3, L0774: 3, L0747: 3, H0668: 3, S0192: 3, H0150: 2, H0620: 2, H0413: 2, H0649: 2, S0426: 2, L0763: 2, L0769: 2, L0648: 2, L0766: 2, L0653: 2, L0657: 2, S0126: 2, H0670: 2, L0754: 2, L0749: 2, H0685: 1, S0040: 1, H0650: 1, S0212: 1, H0255: 1, S0420: 1, S0045: 1, H0261: 1, H0391: 1, L0022: 1, H0581: 1, H0597: 1, H0544: 1, H0545: 1, H0123: 1, H0012: 1, H0024: 1, H0188: 1, S0250: 1,	
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									L0483: 1, H0617: 1, H0551: 1, H0494: 1, S0210: 1, L0372: 1, L0643: 1, L0773: 1, L0803: 1, L0650: 1, L0775: 1, L0375: 1, L0651: 1, L0525: 1, L0776: 1, L0661: 1, L0629: 1, L0664: 1, S0053: 1, L0565: 1, H0690: 1, H0682: 1, H0658: 1, H0648: 1, H0672: 1, H0539: 1, H0521: 1, S0044: 1, S0188: 1, H0555: 1, S3012: 1, L0752: 1, L0753: 1, L0757: 1, L0758: 1, L0592: 1, L0601: 1, L0603: 1 and H0352: 1.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									

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356	HHFGZ38	785591	366	302 - 1165	979				H0663: 2, S0328: 2, S0420: 1, S0046: 1, H0559: 1, T0082: 1, H0050: 1, H0100: 1, H0494: 1, L0640: 1, L0789: 1, H0436: 1 and L0439: 1.		
									AR089: 8, AR061: 2 H0556: 1, S0040: 1, H0657: 1, H0306: 1, H0393: 1, H0050: 1, H0266: 1, H0112: 1, H0063: 1, S0142: 1, S0002: 1, L0794: 1, L0378: 1, L0655: 1, L0791: 1, L0665: 1, H0539: 1, H0521: 1, L0596: 1, L0593: 1, L0595: 1 and H0653: 1.		
357	HDPLN70	854010	367	40 - 828	980	Pro-1 to Gly-7, Arg-15 to Trp-21, Pro-58 to Asn-63, Arg-82 to Gly-88.			AR089: 2, AR061: 1 L0766: 26, L0439: 11, L0757: 8, H0521: 5, L0748: 5, H0462: 4, L0745: 4, L0777: 4, H0013: 3, H0123: 3, L0774: 3, H0522: 3.		

						L0752: 3, S0356: 2, H0261: 2, S0222: 2, H0431: 2, H0427: 2, H0052: 2, H0545: 2, L0770: 2, L0769: 2, L0768: 2, L0806: 2, L0659: 2, H0144: 2, L0751: 2, L0756: 2, L0779: 2, L0591: 2, L0593: 2, H0667: 2, H0677: 2, H0656: 1, H0661: 1, S0358: 1, H0580: 1, S0045: 1, H0370: 1, H0486: 1, H0546: 1, S0022: 1, S0214: 1, H0328: 1, H0615: 1, H0428: 1, T0023: 1, H0628: 1, L0055: 1, H0032: 1, H0090: 1, H0059: 1, H0100: 1, L0351: 1, S0144: 1, S0002: 1, L0598: 1, L0764: 1, L0771: 1, L0662: 1, L0794: 1, L0775: 1, L0805: 1, L0545: 1,				
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									L0543: 1, L0789: 1, L0790: 1, L0791: 1, L0792: 1, L0663: 1, H0520: 1, H0547: 1, H0519: 1, H0648: 1, L0740: 1, L0746: 1, L0747: 1, L0750: 1, L0759: 1, L0608: 1, L0601: 1, S0026: 1, H0665: 1, H0136: 1 and S0242: 1.			
358	HSDIH12	876344	368	3 - 623	981	Thr-1 to Asp-19, Cys-23 to Cys-34, Gln-36 to Gln-58, Leu-78 to Gly-87, Asp-164 to His-169.			AR089: 24, AR061: 6 S0134: 1, L0749: 1, L0759: 1, S0260: 1 and L0596: 1.			
359	HNBT01	913838	369	3 - 827	982	Arg-1 to Gly-10.			AR089: 15, AR061: 5 S0360: 2, L0766: 2, L0747: 2, T0002: 1, H0686: 1, H0662: 1, S0046: 1, H0023: 1, H0560: 1, H0647: 1, L0662: 1, L0666: 1, H0576: 1, L0779: 1, L0596: 1, L0590: 1, L0601: 1 and H0667: 1.			

360	HEOQN14	923752	370	1044 - 520	983		AR089: 15, AR061: 7		
361	HTXKL86	928194	371	1 - 762	984		AR061: 1, AR089: 1 L0438: 12, L0439: 11, H0617: 5, H0556: 4, H0618: 3, H0253: 3, L0769: 3, L0761: 3, L0759: 3, H0544: 2, H0031: 2, H0135: 2, H0038: 2, H0641: 2, L0764: 2, L0783: 2, L0809: 2, L0790: 2, L0666: 2, L0663: 2, L0665: 2, H0144: 2, S0330: 2, L0751: 2, L0779: 2, H0543: 2, H0265: 1, H0685: 1, H0657: 1, H0306: 1, S0420: 1, S0354: 1, S0360: 1, S0046: 1, L0717: 1, H0550: 1, H0592: 1, H0333: 1, H0331: 1, H0559: 1, H0486: 1, H0013: 1, H0244: 1, H0635: 1, H0575: 1, H0596: 1,		

						L0635: 2, L0663: 2, H0697: 2, H0658: 2, S0027: 2, L0740: 2, L0756: 2, L0759: 2, H0445: 2, L0589: 2, L0599: 2, H0170: 1, H0265: 1, H0295: 1, H0583: 1, H0341: 1, H0255: 1, H0459: 1, H0638: 1, H0637: 1, S0045: 1, S6026: 1, H0351: 1, S6016: 1, S0222: 1, H0392: 1, H0574: 1, H0486: 1, H0013: 1, H0250: 1, H0069: 1, H0075: 1, H0427: 1, H0042: 1, H0036: 1, H0004: 1, S0010: 1, T0048: 1, H0318: 1, H0434: 1, H0052: 1, H0086: 1, H0572: 1, H0123: 1, H0012: 1, H0024: 1, S0051: 1, H0594: 1, H0428: 1, H0031: 1, H0165: 1, L0456: 1,
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					H0038: 1, H0634: 1, H0616: 1, H0063: 1, H0551: 1, H0488: 1, S0038: 1, H0130: 1, H0695: 1, L0520: 1, L0640: 1, L0667: 1, L0772: 1, L0764: 1, L0771: 1, L0662: 1, L0363: 1, L0767: 1, L0768: 1, L0803: 1, L0804: 1, L0650: 1, L0805: 1, L0809: 1, H0144: 1, S0310: 1, L0438: 1, L0352: 1, H0660: 1, H0648: 1, H0672: 1, S0330: 1, H0518: 1, H0696: 1, H0187: 1, S3014: 1, S0028: 1, S0032: 1, L0743: 1, L0754: 1, L0746: 1, L0749: 1, L0779: 1, H0343: 1, H0595: 1, L0591: 1, L0592: 1, L0608: 1, L0595: 1, L0366: 1, S0106: 1 and H0352: 1.
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363	HE8TM80	955022	373	358 - 696	986	Arg-1 to Asn-7, Leu-56 to Met-61.	AR089: 9, AR061: 7 H0040: 5, H0547: 5, S0152: 5, L0593: 5, L0595: 5, H0551: 4, H0529: 4, H0519: 4, H0560: 3, H0561: 3, H0657: 2, S0360: 2, S0007: 2, H0586: 2, H0013: 2, H0494: 2, L0809: 2, H0435: 2, S0028: 2, L0748: 2, L0439: 2, L0731: 2, L0759: 2, H0445: 2, L0592: 2, H0542: 2, H0624: 1, H0170: 1, H0556: 1, S0212: 1, H0663: 1, S0418: 1, S0356: 1, S0046: 1, H0393: 1, H0486: 1, H0427: 1, H0156: 1, H0036: 1, H0318: 1, T0110: 1, H0545: 1, H0014: 1, H0266: 1, H0188: 1, S0022: 1, H0328: 1, H0688: 1, T0023: 1, H0032: 1,		
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364	HWLEY40	957875	374	3 - 881	987	Glu-6 to Gly-11, Gly-64 to Ser-70, Val-140 to Val-145, His-163 to Leu-168, Leu-189 to Lys-198, Ser-221 to Thr-227, His-261 to Pro-270.	AR089: 2, AR061: 2, L0438: 12, L0439: 11, H0617: 5, H0556: 4, H0618: 3, H0253: 3, L0769: 3, L0761: 3, L0759: 3, H0544: 2, H0031: 2, H0135: 2, H0038: 2, H0641: 2, L0764: 2, L0783: 2,			H0038: 1, H0268: 1, S0142: 1, S0422: 1, S0426: 1, L0761: 1, L0646: 1, L0765: 1, L0773: 1, L0794: 1, L0766: 1, L0804: 1, L0776: 1, L0655: 1, L0659: 1, L0791: 1, L0792: 1, L0663: 1, L0664: 1, H0666: 1, H0672: 1, H0539: 1, H0555: 1, L0743: 1, L0740: 1, L0749: 1, L0779: 1, L0752: 1, S0026: 1, S0194: 1, H0543: 1, H0423: 1 and S0424: 1.		
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L0809: 2, L0790: 2, L0666: 2, L0663: 2, L0665: 2, H0144: 2, S0330: 2, L0751: 2, L0779: 2, H0543: 2, H0265: 1, H0685: 1, H0657: 1, H0306: 1, S0420: 1, S0354: 1, S0360: 1, S0046: 1, L0717: 1, H0550: 1, H0592: 1, H0333: 1, H0331: 1, H0559: 1, H0486: 1, H0013: 1, H0244: 1, H0635: 1, H0575: 1, H0596: 1, T0110: 1, H0123: 1, H0615: 1, H0033: 1, H0553: 1, H0212: 1, H0124: 1, H0040: 1, H0616: 1, H0264: 1, H0488: 1, H0100: 1, H0494: 1, H0131: 1, H0529: 1, L0637: 1, L0772: 1, L0766: 1, L0775: 1, L0375: 1, L0776: 1, L0628: 1,
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									L0657: 1, L0664: 1, S0374: 1, H0547: 1, H0593: 1, S3014: 1, S0027: 1, L0748: 1, L0750: 1, L0731: 1, L0758: 1, H0595: 1, S0276: 1 and H0423: 1.			
365	HDPPD36	493820	375	403 - 272	988	Trp-22 to Glu-35.			AR089: 1, AR061: 0 H0522: 2, L0439: 2, L0777: 2, H0591: 1, H0144: 1, H0521: 1, L0758: 1 and L0605: 1.			
		964320	620	2 - 436	1233	Met-1 to Tyr-14, Arg-24 to Gly-30, His-49 to Cys-55, Ile-94 to Phe-99, Pro-128 to Gly-136.						
366	H0UBZ94	527876	376	1 - 153	989	Glu-1 to Thr-6.			AR061: 7, AR089: 3 H0161: 1 and S0040: 1.	19p13.3		108725, 120700, 133171, 136836, 145981, 147141, 164953, 188070, 600957,

367	HMIAH32	550977	377	49 - 702	990	His-15 to Ser-21, Asp-44 to Val-65, Glu-95 to Thr-101, Ala-131 to Asp-142.	AR061: 7, AR089: 2 S6028: 2, L0766: 2, L0777: 2, L0752: 2, H0663: 1, H0696: 1 and L0779: 1.	7		601238, 601846, 602216, 602477
368	HDPH43	573418	378	1 - 432	991	Ser-28 to Glu-34, Ser-77 to Arg-82, Trp-127 to Arg-135.	AR061: 2, AR089: 1 S0116: 2, H0586: 1 and H0521: 1.			
369	HCE3W04	615501	379	94 - 873	992		AR089: 1, AR061: 0 L0789: 4, L0731: 4, H0539: 3, L0779: 3, S0007: 2, H0052: 2, L0157: 2, H0123: 2, H0233: 2, L0637: 2, S0356: 1, S0360: 1, H0550: 1, H0253: 1, H0620: 1, H0408: 1, H0188: 1, S0250: 1, L0193: 1, L0455: 1, H0135: 1, H0551: 1, L0770: 1, L0794: 1, L0776: 1, L0665: 1,			

									L0779: 1, H0445: 1 and L0595: 1.			
374	HOQBF64	703177	384	48 - 401	997				AR089: 23, AR061: 14 H0208: 1 and H0290: 1.	17q23-q24	106180, 115660, 138700, 139250, 148500, 150200, 154275, 162100, 170500, 170500, 170500, 176960, 182452, 230200, 249000, 253250	
375	HTEDL38	761609	385	133 - 534	998	Pro-38 to Pro-46.			AR061: 3, AR089: 2 H0038: 4, L0748: 4, S0222: 2, L0598: 2, L0776: 2, L0439: 2, L0780: 2, L0752: 2, H0050: 1, T0006: 1, H0111: 1, S0036: 1, H0616: 1, T0067: 1,			

380	HHEWQ61	876063	390	3 - 497	1003	Thr-6 to Tyr-13, Ala-23 to Asp-30, Phe-66 to Arg-71, Pro-92 to Glu-102, Arg-108 to Leu-116, Tyr-159 to Thr-164.	L0368: 1, S0052: 1, S0146: 1, S0390: 1, S0028: 1 and S0260: 1. AR061: 1, AR089: 0 L0439: 4, H0543: 3, S0360: 2, L0662: 2, L0742: 2, L0481: 1, H0619: 1, H0486: 1, L0586: 1, L0021: 1, S0051: 1, H0424: 1, L0789: 1, S0374: 1, H0539: 1, L0744: 1, L0754: 1, L0777: 1, L0752: 1 and H0506: 1.		
381	HUFGH09	877078	391	3 - 647	1004	Leu-8 to Pro-14, Pro-59 to Asn-64, Pro-80 to Glu-91, Gly-127 to Lys-134, Arg-146 to Glu-152, Thr-156 to Asp-165, Pro-184 to Asp-203.	AR089: 3, AR061: 1 H0624: 2, S0356: 1, H0607: 1, L0060: 1 and H0506: 1.		
382	HLICA79	880881	392	1 - 1197	1005	Arg-1 to Gly-8, Gly-10 to Leu-17, Lys-41 to Pro-51, Lys-67 to Thr-74, Glu-94 to Lys-99,	AR051: 10, AR054: 10, AR050: 9, AR089: 5, AR061: 3 L0775: 4, H0046: 3, H0622: 3, H0660: 3,		

383	HSLIH01	884251	393	11 - 649	1006	Phe-107 to Gly-112, Arg-125 to Glu-131, Leu-141 to Arg-153, Gly-168 to Ala-176, Asn-210 to Arg-215, Asn-222 to Ser-234, Leu-238 to Thr-249.	H0438: 2, L0663: 2, L0665: 2, L0777: 2, S0026: 2, H0583: 1, S0282: 1, S0356: 1, H0051: 1, H0071: 1, H0355: 1, H0510: 1, H0615: 1, H0428: 1, H0644: 1, L0142: 1, S0364: 1, H0059: 1, L0763: 1, L0803: 1, L0804: 1, L0657: 1, L0809: 1, L0664: 1, H0690: 1, H0670: 1, H0672: 1, H0479: 1, S0028: 1, L0751: 1, S0031: 1, L0604: 1, L0366: 1, S0192: 1 and S0424: 1.		
						Arg-14 to Glu-20, Leu-30 to Arg-42, Gly-57 to Ala-65, Asn-99 to Arg-104, Asn-111 to Ser-117.	AR089: 3, AR061: 2, AR051: 2, AR050: 1, AR054: 1 L0775: 4, H0046: 3, H0622: 3, H0660: 3, H0402: 2, H0438: 2, L0663: 2, L0665: 2, L0777: 2, S0026: 2,		

									H0583: 1, S0282: 1, S0356: 1, H0051: 1, H0071: 1, H0355: 1, H0510: 1, H0615: 1, H0428: 1, H0644: 1, L0142: 1, S0364: 1, H0059: 1, L0763: 1, L0803: 1, L0804: 1, L0657: 1, L0809: 1, L0666: 1, L0664: 1, H0144: 1, H0690: 1, H0670: 1, H0672: 1, H0479: 1, S0028: 1, L0751: 1, S0031: 1, L0604: 1, L0366: 1, S0192: 1 and S0424: 1.		
384	HE9OV91	887364	394	34 - 723	1007				AR054: 2, AR051: 2, AR050: 1, AR089: 0, AR061: 0 S0116: 1, H0619: 1, H0421: 1, H0144: 1, L0748: 1 and L0758: 1.		
385	HHEDS85	894602	395	2 - 457	1008	Ser-12 to Ser-19, Ser-34 to Lys-47.			AR061: 2, AR089: 1 T0039: 1, H0144: 1 and H0542: 1.		
386	HNTDJ68	899624	396	667 - 1599	1009	Phe-40 to Tyr-47,			AR051: 25, AR050:		

						Ile-119 to Arg-125, Ser-141 to Arg-200, Arg-217 to Lys-223, Ala-303 to Leu-311.	13, AR089: 3, AR061: 2 L0731: 4, L0596: 4, H0615: 3, L0777: 3, H0625: 2, L0803: 2, L0740: 2, H0657: 1, H0393: 1, H0441: 1, T0109: 1, H0318: 1, H0581: 1, H0566: 1, H0551: 1, L0761: 1, L0641: 1, L0766: 1, L0650: 1, L0784: 1, H0144: 1, H0547: 1, H0539: 1, H0696: 1, S3014: 1, L0744: 1, L0779: 1 and L0780: 1.		
387	HKAHO77	906671	397	712 - 398	1010		AR089: 19, AR061: 7 L0771: 4, L0764: 3, H0282: 2, H0494: 2, L0518: 2, L0617: 1, L0794: 1, L0774: 1, L0806: 1, L0657: 1, L0663: 1, S0374: 1, H0672: 1, L0752: 1 and L0755: 1.		
388	HTFNP84	909687	398	70 - 1227	1011	Tyr-11 to Val-16,	AR089: 0, AR061: 0		

[illegible]

389	HDQGZ78	909735	399	5 - 442	1012	Met-15 to Pro-20, Pro-47 to Arg-53, Tyr-61 to Asp-71.	AR061: 0, AR089: 0 H0521: 2, L0758: 2, H0038: 1, L0644: 1, L0645: 1, L0764: 1, L0662: 1, L0794: 1, L0557: 1, L0747: 1 and	L0520: 1, L0769: 1, L0761: 1, L0764: 1, L0521: 1, L0662: 1, L0774: 1, L0375: 1, L0805: 1, L0776: 1, L0655: 1, L0606: 1, L0659: 1, L0635: 1, L0367: 1, L0789: 1, L0665: 1, H0684: 1, H0670: 1, H0666: 1, H0672: 1, H0521: 1, H0704: 1, S0406: 1, L0439: 1, L0750: 1, L0756: 1, L0779: 1, L0777: 1, L0752: 1, L0755: 1, L0758: 1, L0608: 1, L0362: 1, H0667: 1, S0196: 1, H0543: 1, H0423: 1, H0422: 1 and H0352: 1.		
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390	HHEMD52	909742	400	623 - 1618	1013	Trp-3 to Thr-14, Ala-21 to Arg-30, Glu-66 to Pro-74, Pro-103 to Gly-108, Ile-135 to Ile-142.	L0779: 1. AR089: 4, AR061: 3 H0457: 3, H0271: 3, H0543: 3, H0422: 2, H0583: 1, H0650: 1, H0484: 1, H0483: 1, S0442: 1, H0580: 1, S0140: 1, H0486: 1, H0250: 1, H0050: 1, H0630: 1, H0264: 1, H0488: 1, H0487: 1, S0002: 1, L0439: 1, H0707: 1, H0136: 1 and H0677: 1.		
391	HSIDQ38	909854	401	3 - 764	1014	Ala-18 to Arg-23, Gly-28 to Trp-35, Gln-53 to Arg-61, Asp-122 to Glu-127, Gln-163 to Cys-171.	AR061: 3, AR089: 3 L0766: 5, H0587: 2, H0036: 2, L0745: 2, L0747: 2, H0556: 1, S0114: 1, H0590: 1, H0052: 1, L0640: 1, L0770: 1, L0771: 1, L0659: 1 and L0665: 1.		
392	HSKBF02	909855	402	3 - 395	1015	Gly-35 to Asp-41.	AR089: 53, AR061: 14 L0438: 6, L0751: 6, L0439: 5, L0770: 4, H0052: 2, H0620: 2,		

									H0521: 2, L0756: 2, L0731: 2, L0758: 2, L0588: 2, H0556: 1, S0282: 1, H0662: 1, H0402: 1, S0418: 1, T0008: 1, S0222: 1, H0392: 1, H0333: 1, L0021: 1, H0581: 1, S0049: 1, L0471: 1, H0266: 1, L0351: 1, L0772: 1, L0766: 1, L0776: 1, L0659: 1, L0792: 1, H0522: 1, S0027: 1, L0779: 1 and S0011: 1.				
393	HIBDE74	766011	403	99 - 362	1016				AR089: 1, AR061: 1 L0759: 2, H0171: 1, T0010: 1, H0090: 1, L0761: 1, L0766: 1, S3014: 1, L0745: 1, L0747: 1 and H0506: 1.				
		909876	621	2 - 751	1234								
394	HWMAE53	909877	404	1 - 438	1017			Glu-7 to Gln-17, Tyr-27 to Cys-32, Thr-63 to Lys-70, Glu-89 to Lys-94.	AR089: 3, AR061: 1 S0354: 1 and H0030: 1.				

395	HFXCG28	909961	405	3 - 608	1018	Tyr-100 to Ser-107, Lys-122 to Val-127.	AR061: 3, AR089: 0 S0001: 1, H0619: 1 and H0521: 1.		
396	HFTCU45	910053	406	1 - 504	1019	Glu-47 to Asp-56, Tyr-131 to Gly-136.	AR089: 1, AR061: 0 L0789: 4, H0539: 4, L0731: 4, H0052: 3, L0779: 3, S0007: 2, L0157: 2, H0123: 2, H0233: 2, L0637: 2, S0356: 1, S0360: 1, H0550: 1, H0486: 1, H0013: 1, H0253: 1, H0620: 1, H0408: 1, H0188: 1, S0250: 1, L0193: 1, L0455: 1, H0135: 1, H0551: 1, L0770: 1, L0794: 1, L0776: 1, L0665: 1, S0392: 1, L0750: 1 and L0777: 1.		
397	HFTBL33	910055	407	1 - 1122	1020	Glu-48 to Asp-57.	AR089: 16, AR061: 11 L0789: 4, L0731: 4, H0539: 3, L0779: 3, S0007: 2, H0052: 2,		

									L0157: 2, H0123: 2, H0233: 2, L0637: 2, S0356: 1, S0360: 1, H0550: 1, H0253: 1, H0620: 1, H0408: 1, H0188: 1, S0250: 1, L0193: 1, L0455: 1, H0135: 1, H0551: 1, L0770: 1, L0794: 1, L0776: 1, L0665: 1, S0392: 1, L0750: 1 and L0777: 1.			
398	HTXJA84	911387	408	2 - 628	1021	Arg-1 to Ser-6, Asn-55 to Phe-64, Ser-86 to Gly-92, Leu-124 to Glu-146.			AR061: 5, AR089: 2 H0521: 4, H0457: 3, H0580: 2, L0749: 2, L0588: 2, H0556: 1, H0485: 1, H0635: 1, H0581: 1, H0251: 1, H0124: 1, H0551: 1, H0529: 1, L0667: 1, L0773: 1, L0803: 1, S0052: 1, H0593: 1 and S0424: 1.			
399	HKAAW89	911389	409	1 - 447	1022	Gln-12 to Pro-20, Thr-37 to Glu-42, Ile-49 to Arg-56.			AR089: 0, AR061: 0 H0494: 1, H0520: 1, H0435: 1 and H0423: 1.			

						Leu-75 to Arg-88, Ala-111 to Leu-118.				
400	HSXDD55	911460	410	312 - 737	1023	Arg-75 to Lys-83, Ser-89 to Arg-102, Met-136 to Arg-142.	AR061: 2, AR089: 2 L0439: 2, L0617: 1, S0356: 1, H0457: 1, S0036: 1, H0547: 1, L0758: 1 and L0608: 1.			
401	HUFCI64	911558	411	3 - 773	1024	Ala-89 to Glu-98, Leu-117 to Ala-123, Glu-139 to Gly-147, Leu-158 to Thr-163, Glu-195 to Arg-211.	AR089: 14, AR061: 4 H0436: 11, H0255: 7, H0559: 7, H0521: 7, H0254: 4, H0423: 4, H0265: 3, H0486: 3, H0250: 3, H0581: 3, H0271: 3, H0124: 3, H0264: 3, H0555: 3, H0341: 2, S0354: 2, H0580: 2, H0370: 2, H0586: 2, H0257: 2, H0069: 2, H0083: 2, H0031: 2, H0634: 2, H0488: 2, S0422: 2, S0426: 2, L0766: 2, L0649: 2, L0805: 2, L0653: 2, L0776: 2, L0655: 2, L0731: 2, H0445: 2, H0543: 2,	19p13.3	108725, 120700, 133171, 136836, 145981, 147141, 164953, 188070, 600957, 601238, 601846, 602216, 602477	

402	HWAFT84	911559	412	1 - 702	1025			H0677: 2, H0556: 1, H0584: 1, H0140: 1, H0583: 1, H0656: 1, H0402: 1, H0305: 1, H0458: 1, S0140: 1, H0550: 1, H0497: 1, H0575: 1, S0474: 1, H0421: 1, H0024: 1, H0213: 1, H0087: 1, H0272: 1, H0641: 1, S0144: 1, L0763: 1, L0761: 1, L0662: 1, L0794: 1, L0803: 1, L0804: 1, L0659: 1, L0787: 1, L0666: 1, L0663: 1, H0518: 1, S0044: 1, H0576: 1, L0756: 1, H0422: 1, S0452: 1 and H0506: 1.	AR061: 2, AR089: 1	19p13.3	108725, 120700, 133171, 136836, 145981, 147141, 164953,
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403	HETCL18	914535	413	1 - 684	1026	Lys-12 to Pro-22, Lys-38 to Thr-45, Glu-65 to Lys-70, Phe-78 to Gly-83, Arg-96 to Glu-102, Leu-112 to Arg-124, Gly-139 to Ala-147, Asn-181 to Arg-186, Asn-193 to Ser-205, Leu-209 to Thr-220.	AR054: 8, AR061: 5, AR089: 5, AR050: 1, AR051: 1 L0754: 45, L0747: 8, H0553: 7, L0775: 5, L0755: 5, L0659: 4, H0046: 3, H0622: 3, H0124: 3, L0665: 3, H0660: 3, L0748: 3, L0751: 3, H0402: 2, H0438: 2, H0586: 2, H0427: 2, H0599: 2, H0575: 2, H0050: 2, L0471: 2, H0644: 2, H0616: 2, H0056: 2, L0764: 2, L0662: 2, L0794: 2, L0803: 2, L0804: 2, L0666: 2, L0663: 2, H0144: 2, L0749: 2, L0750: 2,		188070, 600957, 601238, 601846, 602216, 602477
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								S0031: 1, L0605: 1, L0599: 1, L0604: 1, L0603: 1, L0366: 1, S0192: 1, H0543: 1, S0424: 1 and H0506: 1.		
404	HCRNK75	914536	414	2156 - 912	1027	Pro-1 to Met-7, Ala-16 to Gly-24, Gly-26 to Leu-33, Lys-57 to Pro-67, Lys-83 to Thr-90, Glu-110 to Lys-115, Phe-123 to Gly-128, Arg-141 to Glu-147, Leu-157 to Arg-169, Gly-184 to Ala-192, Asn-226 to Arg-231, Asn-238 to Ser-250, Leu-254 to Thr-265.	AR061: 124, AR089: 76 L0775: 4, H0046: 3, H0622: 3, H0660: 3, H0438: 2, L0663: 2, L0665: 2, L0777: 2, S0026: 2, H0583: 1, S0282: 1, S0356: 1, H0051: 1, H0071: 1, H0355: 1, H0510: 1, H0615: 1, H0428: 1, H0644: 1, L0142: 1, S0364: 1, H0059: 1, L0763: 1, L0803: 1, L0804: 1, L0657: 1, L0809: 1, L0664: 1, H0690: 1, H0670: 1, H0672: 1, H0479: 1, S0028: 1, L0751: 1, S0031: 1, L0604: 1, L0366: 1, S0192: 1 and			

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407	HWLFJ01	928017	417	1 - 780	1030	Arg-11 to Arg-19, Ser-36 to Thr-61, Glu-79 to Glu-84, Ala-100 to Gln-106, Ser-155 to Leu-161.	L0753: 1, L0759: 1, H0445: 1, H0595: 1, L0362: 1, H0653: 1 and H0506: 1. AR061: 3, AR089: 2 L0741: 12, L0744: 6, H0052: 5, H0040: 5, L0742: 5, L0748: 5, H0620: 4, L0794: 4, H0486: 3, H0622: 3, L0439: 3, L0749: 3, L0777: 3, S0354: 2, H0046: 2, H0031: 2, H0617: 2, L0770: 2, L0761: 2, L0806: 2, S0126: 2, H0539: 2, H0518: 2, H0521: 2, L0751: 2, L0747: 2, L0758: 2, L0593: 2, H0624: 1, H0171: 1, S0114: 1, H0650: 1, S0418: 1, S0420: 1, H0645: 1, H0351: 1, H0370: 1, H0600: 1, H0592: 1, L0622: 1, T0082: 1, S0474: 1,		
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408	HTXNG95	928577	418	13 - 594	1031	Arg-41 to Thr-53, Ser-89 to Glu-95, Leu-109 to Lys-114, Pro-189 to Glu-194.	H0085: 1, H0235: 1, H0545: 1, H0012: 1, H0644: 1, H0124: 1, H0634: 1, H0494: 1, S0144: 1, S0142: 1, L0638: 1, L0642: 1, L0764: 1, L0771: 1, L0773: 1, L0768: 1, L0649: 1, L0774: 1, L0775: 1, L0651: 1, L0653: 1, L0776: 1, L0659: 1, L0809: 1, S0374: 1, H0690: 1, H0522: 1, H0696: 1, L0740: 1, L0754: 1, L0755: 1, L0731: 1, L0757: 1, H0707: 1, L0601: 1 and H0543: 1.		
							AR054: 26, AR051: 12, AR050: 10, AR061: 7, AR089: 4 H0556: 4, L0770: 4, L0794: 4, L0758: 4, L0731: 3, H0038: 2, L0766: 2, L0659: 2, S0212: 1, S0132: 1,		

									H0632: 1, H0618: 1, H0271: 1, S0368: 1, H0673: 1, L0667: 1, L0662: 1, L0767: 1, L0768: 1, L0381: 1, L0789: 1, L0790: 1, L0664: 1, L0665: 1, H0659: 1, H0658: 1, S0328: 1, S0454: 1, L0749: 1, L0777: 1, H0542: 1 and H0677: 1.			
409	HPCIG66	930886	419	30 - 653	1032	Asn-48 to Gly-54, Thr-56 to Lys-69.			AR089: 1, AR061: 0 H0642: 2 and S0053: 1.			
410	HCRPU72	931140	420	2 - 799	1033	Gly-1 to Val-11, Gly-50 to Thr-62, Asn-125 to Gly-132, Leu-172 to Asn-178, Ser-210 to Ser-217, Ser-232 to Lys-245.			AR089: 16, AR061: 6 H0144: 6, H0013: 2 and S0356: 1.			
411	HE9RT95	934556	421	1 - 714	1034	Leu-21 to Asp-33.			AR089: 17, AR061: 13 S0049: 1, H0144: 1 and L0439: 1.			
412	HFXJM13	935725	422	16 - 438	1035	Gln-36 to Thr-42, Glu-99 to Leu-104.			AR061: 1, AR089: 0 L0748: 7, L0766: 6, L0756: 5, H0580: 4, L0777: 3, H0052: 2,			

		S0051: 2, H0644: 2, H0551: 2, L0769: 2, H0144: 2, L0743: 2, L0754: 2, L0779: 2, L0755: 2, L0759: 2, H0657: 1, H0656: 1, S0116: 1, H0341: 1, S0212: 1, S0282: 1, H0125: 1, L0005: 1, S0222: 1, H0431: 1, H0438: 1, H0586: 1, H0069: 1, H0635: 1, L0157: 1, H0050: 1, L0471: 1, H0051: 1, H0399: 1, H0375: 1, S0318: 1, S0316: 1, H0687: 1, S0250: 1, H0031: 1, H0553: 1, H0090: 1, H0634: 1, H0616: 1, H0623: 1, S0038: 1, H0100: 1, L0371: 1, L0667: 1, L0800: 1, L0794: 1, L0804: 1, L0775: 1, L0805: 1, L0776: 1, L0659: 1, L0526: 1,				
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									L0792: 1, L0663: 1, L0438: 1, H0547: 1, S0126: 1, L0439: 1, L0740: 1, L0749: 1, L0752: 1, S0031: 1, H0445: 1, L0480: 1, L0604: 1, S0026: 1, H0542: 1, S0412: 1 and H0352: 1.			
413	HDPWU37	940705	423	3 - 536	1036	Glu-8 to Pro-17, Pro-31 to Asp-37.	AR089: 12, AR061: 6 H0575: 1, H0271: 1 and H0521: 1.	6 22q13.1	103050, 103050, 124030, 124030, 138981, 182380, 188826, 190040, 190040, 190040			
414	HHSDL85	942246	424	2 - 502	1037	Ser-12 to Gln-25, Pro-29 to Phe-39, Gly-81 to Gly-89, Glu-143 to Trp-156.	AR061: 3, AR089: 2 S0007: 3, S0001: 1, H0618: 1, H0009: 1, S0051: 1, L0763: 1, L0439: 1 and L0758: 1.					
		951168	622	356 - 42	1235	Arg-82 to Trp-88.						
415	HTJMD31	942848	425	1 - 462	1038	Pro-17 to Asn-23.	AR089: 14, AR061: 6					

419	HBXDJ07	946830	429	125 - 652	1042	Glu-62 to Lys-68, Asn-105 to Gly-113.	AR061: 2, AR089: 2 L0439: 11, L0794: 5, L0666: 5, S0222: 4, H0052: 3, L0756: 3, H0624: 2, S6028: 2, S0038: 2, L0638: 2, L0805: 2, L0664: 2, L0438: 2, L0740: 2, H0171: 1, S6024: 1, H0013: 1, H0374: 1, H0050: 1, S0050: 1, H0051: 1, S0386: 1, L0769: 1, L0768: 1, L0776: 1, L0659: 1,	H0013: 1, L0021: 1, H0705: 1, H0150: 1, H0266: 1, H0039: 1, H0622: 1, H0038: 1, H0551: 1, S0422: 1, L0598: 1, L0646: 1, L0766: 1, L0653: 1, L0656: 1, L0789: 1, L0532: 1, L0663: 1, H0658: 1, L0748: 1, L0759: 1, S0434: 1, L0596: 1 and H0506: 1.		
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L0619: 1, H0619: 1, S6026: 1, H0550: 1, H0370: 1, H0600: 1, H0592: 1, H0486: 1, T0040: 1, H0635: 1, H0002: 1, S0010: 1, H0390: 1, H0581: 1, H0421: 1, H0085: 1, T0110: 1, H0041: 1, N0006: 1, H0050: 1, H0012: 1, H0620: 1, T0003: 1, H0024: 1, H0687: 1, H0252: 1, H0604: 1, H0031: 1, H0644: 1, H0628: 1, H0598: 1, H0087: 1, H0264: 1, S0112: 1, T0041: 1, H0560: 1, S0150: 1, H0529: 1, L0640: 1, L0761: 1, L0643: 1, L0806: 1, L0658: 1, L0809: 1, L0544: 1, L0788: 1, L0663: 1, L0664: 1, L0665: 1, S0428: 1, S0053: 1, H0144: 1.
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									H0690: 1, H0518: 1, H0696: 1, H0436: 1, H0576: 1, S0392: 1, L0740: 1, L0731: 1, L0759: 1, S0031: 1, L0596: 1, S0011: 1, H0667: 1 and S0192: 1.			
421	HFKHR40	952470	431	641 - 1756	1044	Gly-18 to His-25.			AR089: 1, AR061: 0 H0457: 7, H0521: 2, H0656: 1, H0458: 1, S0278: 1, H0069: 1, H0620: 1, H0179: 1, H0271: 1, H0416: 1, S0144: 1, H0703: 1, H0593: 1 and H0522: 1.			
422	HDTAI08	953265	432	316 - 567	1045	Leu-13 to Val-25, His-32 to Arg-39.			AR061: 1, AR089: 1 H0521: 4, H0580: 2, H0583: 1, H0486: 1, H0625: 1, S0466: 1, L0666: 1, S0242: 1, H0542: 1 and H0543: 1.			
423	HMKCX80	956254	433	194 - 616	1046	Gln-7 to Asp-19, Leu-34 to Ser-42.			AR089: 7, AR061: 3 H0392: 1, H0427: 1, H0318: 1, L0663: 1, H0345: 1 and L0596: 1.			
424	HCEMF69	961308	434	2 - 637	1047				AR061: 1, AR089: 1			

										S0136: 3, L0779: 3, H0171: 1, H0052: 1, H0038: 1, L0766: 1, H0547: 1, S0031: 1 and S0242: 1.		
425	HWLHF10	963422	435	115 - 978	1048	Ile-44 to Gln-50.				AR089: 26, AR061: 4 S0354: 1, H0561: 1 and L0603: 1.		
426	HOEMG82	963855	436	2 - 991	1049	Asp-1 to Pro-12.				AR061: 49, AR089: 19		
427	HFXDR37	965915	437	1485 - 556	1050	Glu-18 to Thr-23.				AR061: 2, AR089: 1 L0766: 2, S0001: 1, H0592: 1, H0575: 1, H0644: 1, H0038: 1 and H0144: 1.		
428	HNNAS46	969470	438	1 - 834	1051					AR089: 1, AR061: 0 H0638: 2, H0521: 2, L0752: 2, H0677: 2, H0650: 1, H0484: 1, H0458: 1, H0580: 1, H0586: 1, H0575: 1, H0081: 1, S0036: 1, H0063: 1, H0560: 1, L0809: 1, S0126: 1, S0328: 1, L0744: 1, L0740: 1, L0754: 1 and		

429	HRAAS26	971219	439	17 - 535	1052	Glu-25 to Arg-31, Glu-71 to His-76, Leu-85 to Leu-92, Gly-129 to Ser-143.	H0543: 1. AR054: 23, AR050: 18, AR051: 12, AR061: 12, AR089: 8 L0803: 7, L0794: 4, L0748: 4, L0591: 4, L0770: 3, L0804: 3, S0142: 2, L0789: 2, L0743: 2, L0747: 2, L0749: 2, L0752: 2, S0360: 1, S0046: 1, H0549: 1, H0309: 1, H0327: 1, H0012: 1, L0769: 1, L0773: 1, L0767: 1, L0774: 1, L0775: 1, L0776: 1, L0790: 1, L0791: 1, H0435: 1, H0660: 1, H0648: 1, H0521: 1, H0555: 1, L0750: 1, L0779: 1, L0777: 1, L0755: 1, L0758: 1 and S0434: 1.		
430	HHEEL28	973096	440	1 - 378	1053		AR089: 1, AR061: 0 L0766: 7, H0486: 4, L0794: 4, H0520: 4,		

					L0754: 4, L0777: 4, L0755: 4, L0599: 4, L0803: 3, L0779: 3, H0542: 3, H0624: 2, S0418: 2, S0360: 2, H0551: 2, L0770: 2, L0662: 2, L0558: 2, L0665: 2, H0144: 2, H0547: 2, H0519: 2, H0522: 2, L0756: 2, L0758: 2, L0588: 2, H0170: 1, H0556: 1, H0657: 1, H0580: 1, L0717: 1, S0222: 1, H0574: 1, H0599: 1, S0474: 1, H0544: 1, H0266: 1, H0252: 1, T0023: 1, H0553: 1, T0042: 1, S0422: 1, L0369: 1, L0763: 1, L0761: 1, L0772: 1, L0521: 1, L0387: 1, L0650: 1, L0806: 1, L0653: 1, L0655: 1, L0789: 1, L0790: 1, L0663: 1, S0053: 1,		
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431	HCETF22	973324	441	112 - 1863	1054	Asn-1 to Gly-9, Gln-30 to Glu-35.	S0374: 1, H0435: 1, H0670: 1, H0651: 1, H0521: 1, H0436: 1, H0345: 1, L0439: 1, L0745: 1, L0749: 1, L0750: 1, L0759: 1, L0485: 1, L0593: 1, S0026: 1, H0665: 1, H0543: 1, H0423: 1, H0422: 1 and S0458: 1. AR061: 11, AR089: 4 L0741: 8, L0766: 7, L0794: 6, H0306: 4, H0052: 4, L0768: 3, L0803: 3, H0542: 3, S0360: 2, H0457: 2, H0617: 2, H0606: 2, S0036: 2, H0100: 2, L0800: 2, H0672: 2, H0436: 2, L0777: 2, H0543: 2, H0650: 1, L0785: 1, H0341: 1, H0254: 1, H0402: 1, S0420: 1, H0580: 1, S0045: 1, H0645: 1, H0550: 1, S0222: 1,		
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432	HCMSF55	912284	442	657 - 361	1055		S6014: 1, H0592: 1, N0009: 1, S0280: 1, H0599: 1, H0618: 1, S0182: 1, H0581: 1, S0049: 1, H0194: 1, N0007: 1, H0271: 1, H0252: 1, H0063: 1, H0488: 1, H0412: 1, H0079: 1, T0041: 1, H0646: 1, S0144: 1, L0763: 1, L0770: 1, L0769: 1, L0761: 1, L0372: 1, L0646: 1, L0645: 1, L0764: 1, L0774: 1, L0792: 1, L0666: 1, L0665: 1, H0519: 1, H0435: 1, H0539: 1, H0518: 1, L0747: 1, L0755: 1, H0653: 1, H0136: 1, H0677: 1 and S0446: 1.		
							AR089: 2, AR061: 2 L0604: 16, S0366: 9, L0485: 7, L0622: 6, L0623: 6, H0599: 6, H0373: 6, H0196: 4,		

[51] The first column in Table 1A provides the gene number in the application corresponding to the clone identifier. The second column in Table 1A provides a unique "Clone ID NO:Z" for a cDNA clone related to each contig sequence disclosed in Table 1A. This clone ID references the cDNA clone which contains at least the 5' most sequence of the assembled contig and at least a portion of SEQ ID NO:X was determined by directly sequencing the referenced clone. The reference clone may have more sequence than described in the sequence listing or the clone may have less. In the vast majority of cases, however, the clone is believed to encode a full-length polypeptide. In the case where a clone is not full-length, a full-length cDNA can be obtained by methods described elsewhere herein.

[52] The third column in Table 1A provides a unique "Contig ID" identification for each contig sequence. The fourth column provides the "SEQ ID NO:" identifier for each of the contig polynucleotide sequences disclosed in Table 1A. The fifth column, "ORF (From-To)", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence "SEQ ID NO:X" that delineate the preferred open reading frame (ORF) shown in the sequence listing and referenced in Table 1A, column 6, as SEQ ID NO:Y. Where the nucleotide position number "To" is lower than the nucleotide position number "From", the preferred ORF is the reverse complement of the referenced polynucleotide sequence.

[53] The sixth column in Table 1A provides the corresponding SEQ ID NO:Y for the polypeptide sequence encoded by the preferred ORF delineated in column 5. In one embodiment, the invention provides an amino acid sequence comprising, or alternatively consisting of, a polypeptide encoded by the portion of SEQ ID NO:X delineated by "ORF (From-To)". Also provided are polynucleotides encoding such amino acid sequences and the complementary strand thereto.

[54] Column 7 in Table 1A lists residues comprising epitopes contained in the polypeptides encoded by the preferred ORF (SEQ ID NO:Y), as predicted using the algorithm of Jameson and Wolf, (1988) Comp. Appl. Biosci. 4:181-186. The Jameson-Wolf antigenic analysis was performed using the computer program PROTEAN (Version 3.11 for the Power MacIntosh, DNASTAR, Inc., 1228 South Park Street Madison, WI). In specific embodiments, polypeptides of the invention comprise, or alternatively consist of, at least one, two, three, four, five or more of the predicted epitopes as described in Table 1A. It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly.

Column 8 in Table 1A provides an expression profile and library code: count for each of the contig sequences (SEQ ID NO:X) disclosed in Table 1A, which can routinely be combined with the information provided in Table 4 and used to determine the tissues, cells, and/or cell line libraries which predominantly express the polynucleotides of the invention. The first number in column 8 (preceding the colon), represents the tissue/cell source identifier code corresponding to the code and description provided in Table 4. For those identifier codes in which the first two letters are not "AR", the second number in column 8 (following the colon) represents the number of times a sequence corresponding to the reference polynucleotide sequence was identified in the tissue/cell source. Those tissue/cell source identifier codes in which the first two letters are "AR" designate information generated using DNA array technology. Utilizing this technology, cDNAs were amplified by PCR and then transferred, in duplicate, onto the array. Gene expression was assayed through hybridization of first strand cDNA probes to the DNA array. cDNA probes were generated from total RNA extracted from a variety of different tissues and cell lines. Probe synthesis was performed in the presence of ³³P dCTP, using oligo(dT) to prime reverse transcription. After hybridization, high stringency washing conditions were employed to remove non-specific hybrids from the array. The remaining signal, emanating from each gene target, was measured using a Phosphorimager. Gene expression was reported as Phosphor Stimulating Luminescence (PSL) which reflects the level of phosphor signal generated from the probe hybridized to each of the gene targets represented on the array. A local background signal subtraction was performed before the total signal generated from each array was used to normalize gene expression between the different hybridizations. The value presented after "[array code]:" represents the mean of the duplicate values, following background subtraction and probe normalization. One of skill in the art could routinely use this information to identify normal and/or diseased tissue(s) which show a predominant expression pattern of the corresponding polynucleotide of the invention or to identify polynucleotides which show predominant and/or specific tissue and/or cell expression.

Column 9 in Table 1A provides a chromosomal map location for certain polynucleotides of the invention. Chromosomal location was determined by finding exact matches to EST and cDNA sequences contained in the NCBI (National Center for Biotechnology Information) UniGene database. Each sequence in the UniGene database is assigned to a "cluster"; all of the ESTs, cDNAs, and STSs in a cluster are believed to be derived from a single gene. Chromosomal mapping data is often available for one or more

sequence(s) in a UniGene cluster; this data (if consistent) is then applied to the cluster as a whole. Thus, it is possible to infer the chromosomal location of a new polynucleotide sequence by determining its identity with a mapped UniGene cluster.

[57] A modified version of the computer program BLASTN (Altshul et al., J. Mol. Biol. 215:403-410 (1990); and Gish and States, Nat. Genet. 3:266-272 (1993)) was used to search the UniGene database for EST or cDNA sequences that contain exact or near-exact matches to a polynucleotide sequence of the invention (the 'Query'). A sequence from the UniGene database (the 'Subject') was said to be an exact match if it contained a segment of 50 nucleotides in length such that 48 of those nucleotides were in the same order as found in the Query sequence. If all of the matches that met this criteria were in the same UniGene cluster, and mapping data was available for this cluster, it is indicated in Table 1A under the heading "Cytologic Band". Where a cluster had been further localized to a distinct cytologic band, that band is disclosed; where no banding information was available, but the gene had been localized to a single chromosome, the chromosome is disclosed.

[58] Once a presumptive chromosomal location was determined for a polynucleotide of the invention, an associated disease locus was identified by comparison with a database of diseases which have been experimentally associated with genetic loci. The database used was the Morbid Map, derived from OMIM™ (*supra*). If the putative chromosomal location of a polynucleotide of the invention (Query sequence) was associated with a disease in the Morbid Map database, an OMIM reference identification number was noted in column 10, Table 1A, labelled "OMIM Disease Reference(s)". Table 5 is a key to the OMIM reference identification numbers (column 1), and provides a description of the associated disease in Column 2.

TABLE 1B

Clone ID NO:Z	SEQ ID NO:X	CONTIG ID:	BAC ID: A	SEQ ID NO:B	EXON From-To
HFCBB56	24	910073	AC068296	1268	1-225
HIBBF63	75	912715	AC009065	1269	1-70 850-1112 1169-1622 1707-1779 1874-1924 2836-2908 3006-4160
HIBBF63	75	912715	AC012171	1270	1-64 159-209 1122-1194 1292-1527 1593-2446
HIBBF63	75	912715	AC005346	1271	1-70 874-1136 1193-1646 1731-1803 1898-1948 2861-2933 3031-4185
HIBBF63	75	912715	AC009065	1272	1-547
HIBBF63	75	912715	AC012171	1273	1-547
HIBBF63	75	912715	AC009065	1274	1-424
HIBBF63	75	912715	AC005346	1275	1-547
HIBBF63	75	912715	AC012171	1276	1-419
HIBBF63	75	912715	AC005346	1277	1-424
H2CBH45	90	963811	AC068243	1278	1-267 1540-1640 3095-3380 3393-3556 3901-3967 4137-4639 5287-5856 5916-6588 7029-7876 8324-8414
H2CBH45	90	963811	AC068243	1279	1-309
HBGQT03	93	908173	AC024045	1280	1-218

					5744-5972 6327-7067 7097-7152 7210-8073 8079-8680 8772-11399 12956-13517 13736-14155 14311-14753 16294-16357 16648-16806 16874-17059 17685-17787
HCOOZ11	100	965306	AL022238	1286	1-540
HCOOZ11	100	965306	AL022238	1287	1-665
HCWFF88	101	506577	AC025670	1288	1-300
HCWFF88	101	506577	AL157951	1289	1-624
HCWFF88	101	506577	AL157951	1290	1-409
HCWFF88	101	506577	AL157951	1291	1-83
HDPFF24	104	909232	AC020910	1292	1-353 359-468 787-861 1877-2199 4963-5089 5342-5440 6133-8734 9933-10319
HDPFF24	104	909232	AC020910	1293	1-814
HDPFF24	104	909232	AC020910	1294	1-437
HDTKQ14	107	886936	AL359542	1295	1-140 1249-4264
HDTKQ14	107	886936	AL023653	1296	1-140 1249-4264
HDTKQ14	107	886936	AL359542	1297	1-499
HDTKQ14	107	886936	AL359542	1298	1-145
HDTKQ14	107	886936	AL023653	1299	1-499
HFTDF15	113	657020	AL365277	1300	1-406
HFTDF15	113	657020	AC024511	1301	1-406
HFTDF15	113	657020	AL365277	1302	1-430
HFTDF15	113	657020	AC024511	1303	1-430
HFTDF15	113	657020	AL365277	1304	1-526

HFTDF15	113	657020	AC024511	1305	1-526
HLQDT35	117	839777	AC010998	1306	1-44 540-884 1203-1261 1994-2178 2303-2474 2991-3088 3592-3757 4262-4364 4742-5802 6235-7057 7126-8472
HLQDT35	117	839777	AC013357	1307	1-44 540-884 1203-1261 1994-2178 2303-2474 2991-3088 3592-3757 4262-4364 4742-5802 6235-7057 7126-8472
HLQDT35	117	839777	AC010998	1308	1-768
HLQDT35	117	839777	AC013357	1309	1-6035 8430-11057
HLQDT35	117	839777	AC010998	1310	1-278
HLQDT35	117	839777	AC013357	1311	1-278
HLWFN63	118	908437	AC006599	1312	1-30 1525-1711 5428-5502 7038-7273 7590-7735 8960-9049 11665-11800 12889-13194 13907-14119 14889-15043 15926-16164 18759-19079 20581-20693

					22531-22783 23817-24956 26153-26283 26791-27141 28145-29220
HLWFN63	118	908437	AL033378	1313	1-30 1525-1711 5428-5502 7038-7261 7590-7735 11665-11800 12889-13194 13907-14119 14889-15043 15926-16164 18759-19079 20581-20693 22531-22753 23817-24956 26153-26283 26791-27141 28145-29220
HLWFN63	118	908437	AC006599	1314	1-2939
HLWFN63	118	908437	AL033378	1315	1-2939
HMSCD15	120	918133	AC027008	1316	1-1190
HMSCD15	120	918133	AL158207	1317	1-130 923-1252 1765-3269 4138-4483 6546-7734
HMSCD15	120	918133	AL158207	1318	1-371
HPMFL08	128	959569	Z93016	1319	1-477
HPMFL08	128	959569	Z93016	1320	1-650
HTEAG49	135	954614	AL390796	1321	1-1310
HTEAG49	135	954614	AL357045	1322	1-1310
HTEAG49	135	954614	AL390796	1323	1-627
HTEAG49	135	954614	AL357045	1324	1-627
HTLBH67	136	751985	AC008439	1325	1-62 293-400 452-976 1016-1058

					1463-1534 1886-2026 2110-2249 2401-2463 3324-4027 4192-4288 4694-5330 5485-5650 5813-6262 6273-6401 6475-6559 6728-6847 6979-7205 7573-7676 7730-8146 8334-8866 8885-9392
HTLBH67	136	751985	AC008781	1326	1-85 254-371 505-731 1098-1201 1255-1671 1718-2387 2408-2915 3113-3244 3382-4278 4504-4538 4650-5645
HTLBH67	136	751985	AC022420	1327	1-62 295-403 455-979 1019-1061 1466-1537 1890-2030 2114-2253 2405-2467 3328-4030 4195-4291 4697-5333 5488-5653 5816-6265

					6276-6404 6478-6562 6731-6850 6982-7208 7575-7678 7732-8148 8195-8864 8885-9392 9590-9721 9859-10754 10980-11014 11126-12121
HTLBH67	136	751985	AC005368	1328	1-64 294-399 451-975 1015-1057 1462-1533 1885-2025 2109-2248 2400-2462 3323-4026 4191-4287 4693-5329 5484-5649 5812-6264 6275-6403 6477-6561 6730-6849 6981-7207 7575-7678 7732-8148 8201-8868 8887-9394 9592-9723 9861-10759 10985-11019 11131-12126
HTLBH67	136	751985	AC008781	1329	1-292
HTLBH67	136	751985	AC022420	1330	1-323 1372-1431 1657-1821

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					9821-10012
					10197-10277
					10440-10562
					10668-11103
					11203-11432
					11937-12052
					12251-12312
					12794-13183
					13257-13343
					13483-13996
					14001-14146
					14369-14483
					14587-15046
					15053-15302
					15470-15534
					15624-15695
					16128-16212
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					18066-18189
					18298-18394
					18494-18574
					18668-18771
					18896-19043
					19245-19364
					19650-19925
					19968-20102
					20205-20354
					20529-21648
					21748-21816
					21861-22129

22341-22569

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HWWDN34	145	911357	AC019214	1348	1-803 1028-1918
HDPVY89	156	827026	AC026283	1349	1-292 353-776 1340-1506 1568-1696 2408-2534 4767-4955 5472-5546 5957-6293 6373-7085 7386-7445 9201-9273 9532-9672 10470-10641 10873-11481 12131-12705 12990-13214 13351-13509 14119-14173 14445-14570 14879-15004 15604-15844 16133-16253 17540-17867 17944-18254 18356-18755 18892-19002 20066-20352 21146-21308 23235-23486 23813-24533
HDPVY89	156	827026	AC026283	1350	1-318
HFOXK14	180	603245	AL096870	1351	1-68 218-379 706-840

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4074-4162
4353-4422
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4941-5356
5850-5932
6040-6181
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HFOXK14	180	603245	AL096870	1352	1-262
HHFLU06	182	857884	AL096870	1353	1-68 218-379 706-840 1000-1180 1505-2004 2014-2301 3897-3942 4074-4162 4353-4422 4764-4865 4941-5356 5850-5932 6040-6181 6664-6917 7152-7337 7431-7624 8016-8175 8346-8525 9445-9926 10349-10496 10802-10912

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HHFLU06	182	857884	AL096870	1354	1-262
HBIOZ10	187	973131	AC010761	1355	1-543 787-3239 3323-3758 3840-3890
HBIOZ10	187	973131	AC010761	1356	1-134 560-634 971-1091 2351-2501 2711-2875 2967-3126 3298-3461 3575-4655 5184-5345
HBKDI30	188	729048	AL160175	1357	1-155 743-898 1272-1388 4034-4114 4238-4358 4714-4779 4918-5073 5219-5353 6932-7970
HDAAV61	194	810305	AC007136	1358	1-462 1711-2082 4232-4320 4347-4558 4640-4739 7341-7423 7710-8325 8400-8498 8890-9085 9717-9885 10451-10717 10747-10793 11067-13460
HDAAV61	194	810305	AC007136	1359	1-138
HDAAV61	194	810305	AC007136	1360	1-113
HE8UY74	202	960914	AL356968	1361	1-2209
HE8UY74	202	960914	AL356968	1362	1-518

HFKIT06	207	934019	AC068353	1363	1-1562
HFKIT06	207	934019	AC026976	1364	1-222
HFKIT06	207	934019	AC026976	1365	1-294
HFKIT06	207	934019	AF284563	1366	1-1562
HFKIT06	207	934019	AC068353	1367	1-323
HFKIT06	207	934019	AF284563	1368	1-323
HHEHC53	209	921783	AC009427	1369	1-100 1854-1942 3236-3463 4629-4868 5054-5181 5371-5476 5851-5953 6104-6149 6509-6612 7131-8415 8429-8492 8638-8748 8975-9440 9835-10490 10606-10899 11149-11282 11382-11881 12023-12075 12172-12315 12496-12551 12638-12706 12827-12994 13077-13630
HHEHC53	209	921783	AC009427	1370	1-428
HHEHC53	209	921783	AC009427	1371	1-388 466-526 698-906 1023-1922
HMTAJ73	215	813296	AC015698	1372	1-132 337-470 573-666 1313-1765 1962-2257 2433-2599 2611-2991

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HMTAJ73	215	813296	AC015698	1373	1-184
HNTMD79	217	934522	AL160291	1374	1-240 824-922 1460-1771 3163-3311 4244-4385 5252-5359 5721-5781
HNTMD79	217	934522	AL365228	1375	1-240 1460-1771 3163-3311 4244-4385 5253-5360 5722-5782
HNTMD79	217	934522	AL160291	1376	1-694
HNTMD79	217	934522	AL365228	1377	1-694
HNTNB14	219	909942	AC068701	1378	1-414 578-660 871-957 1247-1581 1647-3915
HNTNB14	219	909942	AC068701	1379	1-148
HTEMU66	232	944419	AL022167	1380	1-1796
HTEMU66	232	944419	AC018903	1381	1-631
HTEMU66	232	944419	AC068470	1382	1-706
HTEMU66	232	944419	AL049186	1383	1-912
HTEMU66	232	944419	AC006510	1384	1-1150
HTEMU66	232	944419	AC022305	1385	1-686
HTEMU66	232	944419	AL049186	1386	1-87
HTPGG25	239	911282	AC020705	1387	1-125 455-594 711-853 934-1082 1618-1727 2487-2898 3420-3558
HTPGG25	239	911282	AC020705	1388	1-924 1085-2662
HWAFG04	244	952878	AC018571	1389	1-36 150-275

HHPDV86	310	522953	AC025928	1399	1-62 370-633 1054-1403 1500-1650 1962-2043 2080-2494 2660-2823 3015-3150 5002-5160 5681-5758 7238-7722 7759-8092 8289-8396 8800-9692
HHPDV86	310	522953	AL109627	1400	1-62 374-637 1058-1406 1503-1653 1965-2046 2083-2497 2663-2826 3018-3153 5010-5168 5723-5800 7279-7763 7800-8131 8328-8435 8839-9730
HHPDV86	310	522953	AC025928	1401	1-137 3556-3999 4417-4578
HHPDV86	310	522953	AL109627	1402	1-137 3556-3999 4417-4578
HTTKF86	318	912689	Z82188	1403	1-128 933-996 1532-1699 6031-7667
HTTKF86	318	912689	Z82188	1404	1-282
HTTKF86	318	912689	Z82188	1405	1-896
HCESA79	319	912709	AC009065	1406	1-70

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HCESA79	319	912709	AC012171	1407	1-64 159-209 1122-1194 1292-1527 1593-2446
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HCESA79	319	912709	AC009065	1409	1-547
HCESA79	319	912709	AC012171	1410	1-547
HCESA79	319	912709	AC009065	1411	1-424
HCESA79	319	912709	AC005346	1412	1-547
HCESA79	319	912709	AC012171	1413	1-419
HCESA79	319	912709	AC005346	1414	1-424
HDTBJ28	320	912714	AP001793	1415	1-791 2172-2708 3318-3396
HDTBJ28	320	912714	AP000864	1416	1-973 2292-2890 3500-3585
HDTBJ28	320	912714	AC008052	1417	1-1228 2610-3146 3756-3852 6044-6512
HDTBJ28	320	912714	AC015676	1418	1-782 2163-2699 3310-3406 5603-6071
HDTBJ28	320	912714	AC008052	1419	1-281 344-1073 1346-1846

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HMCAV88	347	924874	AL357752	1434	1-77 341-747 965-1229 1420-1508 1759-1820 2099-2206 2596-2659 2805-3342
HMCAV88	347	924874	AC005476	1435	1-960
HMCAV88	347	924874	AC068231	1436	1-202 2270-2941 5541-5653 5766-5910 6198-6242
HMCAV88	347	924874	AC068231	1437	1-415 674-737 960-1053 1379-1496
HMCAV88	347	924874	AL357752	1438	1-415 674-737 960-1053 1379-1496
HMCAV88	347	924874	AC005476	1439	1-366
HFVHV40	349	945849	AC020911	1440	1-149 3465-3490 3536-3663 5417-6105 6912-7217 8423-8493 8847-9176 10098-10233 10536-11336
HFVHV40	349	945849	AC020911	1441	1-299
HFVHV40	349	945849	AC020911	1442	1-110
HEAAE08	351	959970	AC008687	1443	1-66 297-597

					884-1115 1668-2115 2645-2819 2847-3188 3247-3306 3480-4766
HEAAE08	351	959970	AC008687	1444	1-95
HAPRM21	353	963200	AL034374	1445	1-78 996-1169 2915-3039 3204-3252 3307-3664 4437-4671 4859-4972 5431-8861
HAPRM21	353	963200	AL034374	1446	1-498
HAPRM21	353	963200	AL034374	1447	1-495
HTADZ74	358	811489	AC007278	1448	1-164 1470-1572 1892-2030 3973-4099 5671-5845 6588-7389
HAPNZ77	359	887072	AC076973	1449	1-480
HAPNZ77	359	887072	AC023098	1450	1-1520 1808-2468
HAPNZ77	359	887072	AC003046	1451	1-3893 4181-4841
HAPNZ77	359	887072	AC005859	1452	1-3893 4181-4841
HAPNZ77	359	887072	AC023098	1453	1-307
HTSFJ40	364	722406	AC006171	1454	1-247 1217-1320 1624-1963 2076-2179 2604-2711 2716-3114 3399-3638 4344-4427 5079-5141 5439-8153

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HTSFJ40	364	722406	AL161645	1455	1-247 1217-1320 1624-1963 2076-2179 2604-2711 2716-3114 3399-3638 4344-4427 5079-5141 5439-8153 8268-8798
HTSFJ40	364	722406	AC006171	1456	1-2213
HSDJH12	368	876344	AC021747	1457	1-76 239-328 886-973 3912-4047 6397-6453 7393-7574 8590-9069 9354-10839 13386-13803 14791-15108 15296-15408 15499-15925 16031-16317 16452-16602 17145-18449
HSDJH12	368	876344	AL359882	1458	1-283 1271-1588 1793-1888 1979-2405
HSDJH12	368	876344	AC046143	1459	1-283 1272-1589 1794-1889 1980-2406 2512-2797 2932-3082
HWLEY40	374	957875	AC006171	1460	1-247 1217-1320 1624-1963

					7283-7430 7520-7600 7693-7860 8181-8524 8634-8807 8902-9116 9783-10438 10525-11054 11241-11936 11948-12010 12111-12748 13154-13362 13540-13833 14748-14851 14928-15142 15543-15616 17091-17240 17351-18020 18331-18662 19524-19871 19999-20209 20570-20670 20861-21075 22489-22727 22961-23073 25307-25360 29573-29961 31051-31168
HOUBZ94	376	527876	AC005954	1465	1-131
HCE3W04	379	615501	AC022366	1466	1-565 1503-1718 1838-1933 2011-2097 2265-2335 2588-2693 2905-2975 3090-3726 3809-3889 4080-4591 4847-5070 5355-5819

HCE3W04	379	615501	AC022506	1467	1-563 1501-1716 1836-1931 2009-2094 2263-2333 2586-2691 2903-2973 3088-3724 3807-3887 4085-4540
HCE3W04	379	615501	AC025165	1468	1-565 1503-1718 1838-1933 2011-2097 2265-2335 2588-2693 2905-2975 3090-3726 3809-3889 4080-4591 4847-5070 5355-5819
HCE3W04	379	615501	AC025165	1469	1-604
HCE3W04	379	615501	AC022506	1470	1-518 999-1533 1563-1830 2015-2094 2441-3538 4095-4315 4655-5378
HPJAP28	382	686349	AC004794	1471	1-599 769-987 1562-1690 1879-2043 2595-2821 3807-5923 6102-6572 6644-7502 8127-8585 9415-9553 9669-9763

					9826-9989 10230-10322
HPJAP28	382	686349	AC004794	1472	1-97 1121-1975
HPJAP28	382	686349	AC004794	1473	1-691
HIBEC79	383	703000	AC011458	1474	1-138 397-1114 1356-1693 1781-2091 2270-2389 2474-2908 3053-3202 3288-3349 3421-3976 4551-4662 4696-5053 5166-5246 5318-5490 5592-5723 6082-6283 6619-6733 6853-6942 7491-7586 7922-8003 8015-8421 8432-8624 8714-8856 8943-10332 10482-10901 11647-11934 13110-13177 13310-14175
HIBEC79	383	703000	AC011458	1475	1-406
HIBEC79	383	703000	AC011458	1476	1-287
HNFS82	387	779946	AC010835	1477	1-418
HFPBB28	389	844526	AC016135	1478	1-845
HFPBB28	389	844526	AC018512	1479	1-776
HFPBB28	389	844526	AC073717	1480	1-240
HFPBB28	389	844526	AC002518	1481	1-150
HDQGZ78	399	909735	AC026282	1482	1-238 976-1440

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					2143-2356 6769-6910 9591-9648 9951-10098
HSIDQ38	401	909854	AC003070	1483	1-152 3039-3473 4301-4483 4678-4795 5280-5944 6055-6117 6290-6359 6677-6761 8475-9284 11404-11918 12112-12437 12443-13065 13153-13467 13593-13719 13799-14185 14224-16489
HFTBL33	407	910055	AC022366	1484	1-565 1503-1718 1838-1933 2011-2097 2265-2335 2588-2693 2905-2975 3090-3726 3809-3889 4080-4591 4847-5070 5355-5819
HFTBL33	407	910055	AC025165	1485	1-565 1503-1718 1838-1933 2011-2097 2265-2335 2588-2693 2905-2975 3090-3726 3809-3889

					4080-4591 4847-5070 5355-5819
HFTBL33	407	910055	AC025165	1486	1-604
HUFCI64	411	911558	AC004151	1487	1-145 359-443 527-599 798-868 958-1095 1196-1260 1465-1577 1652-1732 2256-3158 4031-4899 4984-5306 5735-6066 6554-6694 6780-6970 7107-7232 7316-7404 7529-7643 7744-7917 8401-8592 8675-8813 9685-9920 9958-10211 10485-11014 11088-11199 11958-15576 16324-16465 16587-16818 16939-17000 17440-17554 17558-17946 18645-18765 19015-19378 20522-20937 22111-22452
HUFCI64	411	911558	AC004151	1488	1-134
HWAFT84	412	911559	AC004151	1489	1-145 359-443

					4267-4381 4704-4736
HWADR60	416	926487	AC023176	1492	1-162 443-739 1067-1458 1745-1877 1976-2119 2816-2883 3171-3294 3727-4154 4340-4442 5251-6126 6708-7176 7418-7880 8134-8752 9979-10164 11234-11413 12532-12666 13313-13459 14761-14898 15208-15308 16207-16518
HPCIG66	419	930886	AC024888	1493	1-36 149-234 537-623 852-921 1077-1728
HPCIG66	419	930886	AC024888	1494	1-61 133-210 992-1107 1310-1644 1834-1905 2133-2254 2927-3032 4154-4254 4482-4683
HPCIG66	419	930886	AC024888	1495	1-63 239-327 574-1064 1763-2190 2394-2604

					2659-2795 3452-4040 5967-6046 6187-6254
HCRPU72	420	931140	AC023151	1496	1-65 721-1042
HE9RT95	421	934556	AC008439	1497	1-57 311-418 1581-1904 2176-2322 2625-2690 3445-3950 5254-5425 5466-5980 6002-6037 6169-6228 6339-6480 6701-6739 7238-7349 7664-8821
HE9RT95	421	934556	AC022420	1498	1-323 1372-1431 1657-1821 2377-2485 4488-4700 4954-5061 6224-6547 6819-6965 7268-7333 8088-8593 9897-10068 10109-10623 10645-10680 10812-10871 10982-11123 11345-11383 11877-12000 12310-13467
HE9RT95	421	934556	AC022420	1499	1-389
HE9RT95	421	934556	AC022420	1500	1-62 295-403

					455-979 1019-1061 1466-1537 1890-2030 2114-2253 2405-2467 3328-4030 4195-4291 4697-5333 5488-5653 5816-6265 6276-6404 6478-6562 6731-6850 6982-7208 7575-7678 7732-8148 8195-8864 8885-9392 9590-9721 9859-10754 10980-11014 11126-12121
HWADD57	426	943039	AC011492	1501	1-303 949-1648 1913-2937 3032-3231 3325-3443 4093-4485 4777-4936 5057-5548 5650-5968
HWADD57	426	943039	AC011492	1502	1-50 852-907 988-1407 1584-1839 2455-2586 2689-2787
HFKHR40	431	952470	AC018805	1503	1-525 612-1372 1476-1730

10240" 3334360

					1732-2155 2345-2460 2652-3025 3157-3251 3449-3540 3680-3780 3914-4131 4215-4491 4603-4741 4913-4987 5135-5190 5435-5571 5901-6011 6309-6423 6922-8294 8370-8522
HFKHR40	431	952470	AC061707	1504	1-527 614-1374 1478-1732 1734-2158 2348-2463 2655-3027 3159-3253 3451-3542 3682-3782 3916-4134 4219-4495 4607-4745 4917-4991 5139-5194 5439-5575 5905-6015 6313-6427 6926-9300 9919-9960 10029-10186 11393-11624 12094-12294 13227-13375 13690-13829 13921-14010

14362-14486

					14362-14486
HFKHR40	431	952470	AC018805	1505	1-343 700-770
HFKHR40	431	952470	AC061707	1506	1-343 700-771
HFKHR40	431	952470	AC061707	1507	1-277
HWLHF10	435	963422	AC010545	1508	1-40 1661-1891 2119-2199 5160-5349 6239-6607 7675-8566 9450-9516 9675-9752 10110-10274 14154-15055 16384-16500 17055-17139 19941-20453 20703-21216 21806-21945 23638-24171 24527-24795 25564-25656 26644-26787 27284-27438 28354-28612 29247-29591 29597-30208 32018-32539 33187-33942
HWLHF10	435	963422	AC010545	1509	1-721
HWLHF10	435	963422	AC010545	1510	1-610 675-1454 1591-2267 2801-3363

[59] Table 1B summarizes additional polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) contig nucleotide sequence identifiers (SEQ ID NO:X)), and genomic sequences (SEQ ID NO:B). The first column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence. The second column provides the sequence identifier, "SEQ ID NO:X", for each contig sequence. The third column provides a unique contig identifier, "Contig ID:" for each contig sequence. The fourth column, provides a BAC identifier "BAC ID NO:A" for the BAC clone referenced in the corresponding row of the table. The fifth column provides the nucleotide sequence identifier, "SEQ ID NO:B" for a fragment of the BAC clone identified in column four of the corresponding row of the table. The sixth column, "Exon From-To", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:B which delineate certain polynucleotides of the invention that are also exemplary members of polynucleotide sequences that encode polypeptides of the invention (e.g., polypeptides containing amino acid sequences encoded by the polynucleotide sequences delineated in column six, and fragments and variants thereof).

TABLE 2

Clone ID NO:Z	Contig ID:	SEQ ID NO:X	Analysis Method	PFam/NR Description	PFam/NR Accession Number	Score/ Percent Identity	NT From	NT To
HDPTE21	1165861	11	blastx.14	(AB018414) Gab2 [Mus musculus]	gi 4589377 dbj BAA7 6738.1	74% 50% 55% 65% 68% 69% 66% 39% 32% 45% 36% 34%	51 246 1650 1344 1620 1188 1260 1527 1017 1182 1528 2907	227 416 1784 1421 1667 1226 1295 1595 1100 1241 1584 2984
HDPTE21	887711	443	HMMER 2.1.1	PFAM: PH domain	PF00169	25.2	31	129
H6EDR51	930788	445	HMMER 2.1.1	PFAM: PH domain	PF00169	80.9	664	951
			blastx.2	(AF053974) SWAP-70 [Mus musculus]	gb AAC40155.1	53% 57% 26% 19% 43% 33%	19 1291 1464 1566 1199 1214	996 1395 1760 1826 1279 1285
HAPRA41	1154054	13	blastx.14	actin filament-associated protein [Gallus gallus]	gi 487418 gb AAA18 166.1	82%	53	1261
HAPRA41	926285	446	HMMER 2.1.1	PFAM: PH domain	PF00169	59.8	111	398

HBXBI07	954118	447	blastx.2	actin filament-associated protein [Gallus gallus] PFAM: PH domain	gb AAA18166.1	76%	45	473
HBXCM38	910086	15	HMMER 2.1.1	PFAM: PH domain	PF00169	33.2	164	484
			blastx.2	(AF101054) PHR1 isoform 2 [Homo sapiens]	gb AAF18572.1 AF101054_1	100% 92%	119 684	637 722
HCE3E50	961098	448	HMMER 1.8	PFAM: Src homology domain 3	PF00018	55.89	1062	1232
			blastx.2	unnamed protein product [unidentified]	emb CAB69447.1	92% 87% 77%	402 13 1295	1316 396 1348
HCEQD04	1150868	17	HMMER 1.8	PFAM: PH (pleckstrin homology) domain	PF00169	50.5	146	448
			blastx.14	(AF163255) adaptor protein DAPP1 [Mus musculus]	gi 5733602 gb AAD49698.1 AF163255_1	36%	30	278
HCEQD04	927873	449	HMMER 2.1.1	PFAM: PH domain	PF00169	44.9	139	258
			blastx.2	(AF163255) adaptor protein DAPP1 [Mus musculus]	gb AAD49698.1 AF163255_1	37%	7	270
HDPHI92	909900	18	HMMER 2.1.1	PFAM: RhoGAP domain	PF00620	235.1	888	1343
			blastx.2	racGAP [Dictyostelium discoideum]	emb CAA71241.1	37%	825	1343
HDPLT89	962403	19	HMMER 2.1.1	PFAM: Src homology domain 2	PF00017	85.1	194	418
			blastx.2	(AF163254) adaptor protein DAPP1 [Homo sapiens]	gb AAD49697.1 AF163254_1	100%	92	931
HDPSU48	1228284	20	blastx.14	hypothetical protein	pir T13601 T13601	56%	421	873

				80H7.5 - fruit fly (Drosophila melanogaster)				72%	243	485
HDPSU48	909949	450	HMMER 2.1.1 blastx.2	PFAM: FYVE zinc finger	PF01363			101.5	668	868
				(AL031027) /prediction=(method:""ge nefinder"", 1 1 1 PROTEIN)"", sp	emb CAA19842.1			70%	230	862
HDPWE80	909916	21	HMMER 2.1.1 blastx.2	PFAM: PH domain	PF00169			81.2	412	708
				(AF102854) membrane- associated guanylate kinase-interacting protein 2 Maguin-2 [Rattus norvegicus]	gb AAD04568.1			36%	349	756
HDQFY84	971615	451	HMMER 2.1.1	PFAM: PH domain	PF00169			52.1	1232	1507
HEONQ19	930705	23	HMMER 2.1.1 blastx.2	PFAM: PH domain	PF00169			42.5	213	533
				(AJ250425) Collybistin I [Rattus norvegicus]	emb CAB65966.1			96%	9	629
HFCBB56	910073	24	HMMER 1.8 blastx.2	PFAM: EF hand	PF00036			23.95	431	514
				1-phosphatidylinositol- 4,5-bisphosphate phosphodiesterase 1	pir S14113 S14113			36%	275	565
HFKKZ94	926486	452	HMMER 2.1.1	PFAM: PH domain	PF00169			55.3	226	558
HHBGJ53	909912	453	HMMER 2.1.1	PFAM: PH domain	PF00169			38.3	160	267
HHFJF24	1212624	27	blastx.14	GUANINE	sp Q64096 DBS MO			83%	3	566

				NUCLEOTIDE EXCHANGE FACTOR DBS (DBLS BIG SISTER) (MCF2 TRANSFORMING SEQUENCE-LIKE PROTEIN).	USE	71% 79% 23%	545 878 512	811 979 613
HHFJF24	910065	454	HMMER 1.8 blastx.2	PFAM: PH (pleckstrin homology) domain GUANINE NUCLEOTIDE EXCHANGE FACTOR DBS (DBL'S BIG SISTER) 1 (FRAGMENT).	PF00169 sp Q63406 DBS_RA T	23.24 98%	3 3	107 158
HHFMM10	1178801	28	blastx.14	putative [Rattus norvegicus]	gi 397579 emb CAA5 2297.1	97% 91%	138 503	263 613
HHFMM10	962997	455	HMMER 2.1.1 blastx.2	PFAM: PH domain putative [Rattus norvegicus]	PF00169 emb CAA52297.1	42.9 95%	251 131	487 493
HHPBA42	901921	29	HMMER 2.1.1 blastx.2	PFAM: PH domain mitogen inducible gene mig-2 [Homo sapiens]	PF00169 emb CAA80852.1	42.4 61%	352 1	663 822
HHPSP89	910024	456	HMMER 2.1.1 blastx.2	PFAM: PH domain (AB023656) KIF1B-beta [Mus musculus]	PF00169 dbj BAA75243.1	62.3 87%	562 118	855 906
HKABX13	1167182	31	blastx.14	(AK000790) unnamed protein product [Homo sapiens]	gi 7021093 dbj BAA9 1379.1	98% 57%	97 589	480 786

HKABX13	958656	457	HMMER 1.8 blastx.2	PFAM: PH (pleckstrin homology) domain (AK000790) unnamed protein product [Homo sapiens]	PF00169 dbj BAA91379.1	51.8	104	424
HLTHG77	878592	458	HMMER 2.1.1 blastx.2	PFAM: PH domain (AK001472) unnamed protein product [Homo sapiens]	PF00169 dbj BAA91711.1	60.2	1254	1625
HLWBZ09	957912	459	HMMER 1.8	PFAM: PH (pleckstrin homology) domain	PF00169	21.29	145	417
HLWEH54	932133	460	HMMER 2.1.1	PFAM: PH domain	PF00169	114.1	556	849
HL YAA41	1188029	35	blastx.14	SecG [Dictyostelium discoideum]	gi 1688318 gb AAB3 6958.1	43%	173	352
HL YAA41	909874	461	HMMER 2.1.1	PFAM: PH domain	PF00169	37.3	162	260
HL YDV62	1154065	36	blastx.14	SecG [Dictyostelium discoideum]	gi 1688318 gb AAB3 6958.1	43%	173	352
HL YDV62	927872	462	HMMER 2.1.1 blastx.2	PFAM: PH domain (AC005496) unknown protein [Arabidopsis thaliana]	PF00169 gb AAC35236.1	58.6	188	406
HMCFB47	910088	463	HMMER 2.1.1 blastx.2	PFAM: PH domain (AB005903) AtPH1 [Arabidopsis thaliana]	PF00169 dbj BAA84651.1	73	79	378
HMSOI20	928168	464	HMMER 1.8	PFAM: PH (pleckstrin homology) domain	PF00169	30%	85	375
						18.44	154	384

HOENH55	1163460	39	blastx.14	p116Rip [Mus musculus]	gi 1657837 gb AAB18198.1	95% 86% 100% 80% 40%	343 1 139 220 293	624 90 207 294 358
HOENH55	922141	465	HMMER 2.1.1	PFAM: PH domain	PF00169	50.5	406	621
HPIAI01	1078178	40	blastx.2 blastx.14	p116Rip [Mus musculus] unnamed protein product [unidentified]	gb AAB18198.1 gi 4756912 emb CAB42323.1	76% 36% 42% 72%	1 213 414 183	624 437 476 215
HPIAI01	909928	466	HMMER 2.1.1	PFAM: PH domain	PF00169	30.3	294	482
HPJCT50	919836	467	blastx.2 HMMER 2.1.1	unnamed protein product [unidentified] PFAM: PH domain	emb CAB42187.1 PF00169	62% 81.4	10 728	195 1015
HPMFE91	1164740	42	blastx.2 blastx.14	(AF210818) SWAP-70 [Homo sapiens] (AF136450) goodpasture antigen-binding protein [Homo sapiens]	gb AAF24486.1 AF210818_1 gi 4835895 gb AAD30288.1 AF136450_1	85% 89% 97%	98 20 1097	1453 1129 1813
HPMFE91	910026	468	HMMER 2.1.1	PFAM: PH domain	PF00169	81.9	332	613
HRAED51	1090522	43	blastx.2 blastx.14	(AF136450) goodpasture antigen-binding protein [Homo sapiens] racGAP [Dictyostelium discoideum]	gb AAD30288.1 AF136450_1 gi 2190355 emb CAA71241.1	94% 40% 48%	263 363 195	955 569 305
HRAED51	909859	469	HMMER 2.1.1	PFAM: RhoGAP domain	PF00620	78.3	259	504

			blastx.2	beta-chimaerin [Rattus norvegicus]	gb AAA40809.1	28%	259	585
HSMBA19	924885	470	HMMER 2.1.1	PFAM: PH domain	PF00169	34.3	289	528
			blastx.2	(AL096767) dJ579N16.2 (SET binding factor 1) [Homo sapiens]	emb CAB63063.1	49% 76%	4 533	531 607
HSYCY88	914775	45	HMMER 2.1.1	PFAM: PH domain	PF00169	34.6	811	966
			blastx.2	putative [Rattus norvegicus]	emb CAA52297.1	97% 63% 88% 50% 44%	607 21 425 962 1041	966 437 532 1111 1136
HTEDW26	909749	46	HMMER 2.1.1	PFAM: FYVE zinc finger	PF01363	88.9	321	521
			blastx.2	(AF038388) actin-filament binding protein Frabin [Rattus norvegicus]	gb AAC27698.1	89% 51%	57 1	959 81
HTEKD92	1090524	47	blastx.14	(AK000074) unnamed protein product [Homo sapiens]	gi 7019925 dbj BAA90927.1	87%	482	1165
HTEKD92	910027	471	HMMER 2.1.1	PFAM: PH domain	PF00169	54.1	252	530
			blastx.2	(AK000074) unnamed protein product [Homo sapiens]	dbj BAA90927.1	87%	468	1151
HTLDT05	909752	472	HMMER 2.1.1	PFAM: PH domain	PF00169	36.9	59	271
			blastx.2	(AK000004) FLJ00004 protein [Homo sapiens]	dbj BAA92229.1	77%	47	487

HTPDS90	529764	473	HMMER 2.1.1 blastx.2	PFAM: PH domain putative [Rattus norvegicus]	PF00169 emb CAA52297.1	65.3 79% 65%	132 75 2	440 458 58
HTPHM71	1194698	50	blastx.14	CDNA FLJ20260 FIS, CLONE COLF7627.	sp BAA91043 BAA9 1043	62% 70% 42% 59% 47% 23% 42% 80% 27% 38%	61 1423 520 1192 700 889 1054 808 1552 600	348 1659 675 1287 762 1002 1131 837 1671 653
HTPHM71	909878	474	HMMER 1.8 blastx.2	PFAM: PH (pleckstrin homology) domain (AK00267) unnamed protein product [Homo sapiens]	PF00169 dbj BAA91043.1	38.8 53% 31% 65% 32% 42%	57 6 711 1139 550 957	341 341 929 1207 690 1034
HUUAR12	944393	475	HMMER 2.1.1 blastx.2	PFAM: PH domain (AB008430) CDEP [Homo sapiens]	PF00169 dbj BAA24267.1	63.5 45%	69 3	359 677
HWAGP22	1150195	52	blastx.14	(AL031027) /prediction=(method:""ge nfinder"", 1 1 1 PROTEIN)"", sp	gi 3292902 emb CAA 19842.1	50%	1653	1021
HWAGP22	909919	476	HMMER 2.1.1 blastx.2	PFAM: FYVE zinc finger (AL031027)	PF01363 emb CAA19842.1	89.9 50%	516 78	716 710

				/prediction=(method:""ge nefinder"" , 1 1 1 PROTEIN)"" , sp				
HWBCE37	906968	53	HMMER 1.8	PFAM: PH (pleckstrin homology) domain	PF00169	60.73	39	353
			blastx.2	brain beta spectrin [Mus musculus]	gb AAC42040.1	30%	93	386
HWLFB60	1223499	54	blastx.14	CG1513 PROTEIN.	sp Q9V5D4 Q9V5D4	64%	1445	1924
						72%	1127	1459
						66%	2	355
						33%	1943	2218
						52%	518	580
						24%	1295	1393
						38%	89	142
HWLFB60	910018	477	HMMER 2.1.1	PFAM: PH domain	PF00169	43	8	241
			blastx.2	(AF000195) Contains similarity to Pfam domain: PF00169 (PH), 1	gb AAC24270.1	63%	14	241
						33%	238	414
HDPGS16	909833	478	HMMER 1.8	PFAM: Protein kinase C terminal domain	PF00433	57.51	287	445
			blastx.2	(AJ245709) Akt-3 protein [Homo sapiens]	emb CAB53537.1	100%	236	460
						100%	3	116
HDQDV69	937850	56	HMMER 2.1.1	PFAM: Eukaryotic protein kinase domain	PF00069	212.5	68	598
			blastx.2	(AF169035) protein kinase [Homo sapiens]	gb AAF12758.1 AF1 69035_1	98%	68	829
HE6BK63	1153879	57	blastx.14	(AF128625) CDC42- binding protein kinase beta [Homo sapiens]	gi 5006445 gb AAD3 7506.1 AF128625_1	99%	6	767
HE6BK63	661045	480	HMMER	PFAM: Protein kinase C	PF00433	21.1	679	765

			2.1.1	terminal domain	gb AAD37506.1 AF1 28625_1	97%	589	1179
			blastx.2	(AF128625) CDC42- binding protein kinase beta [Homo sapiens]		99%	101	595
						23%	862	1152
						18%	922	1140
						25%	937	1152
						22%	934	1170
						22%	904	1161
HE6BK63	974253	481	blastx.14	(AF128625) CDC42- binding protein kinase beta [Homo sapiens]	gi 5006445 gb AAD3 7506.1 AF128625_1	99%	2	328
						66%	357	500
						100%	502	570
						22%	137	325
						100%	330	362
						55%	325	378
						32%	242	325
						53%	523	561
HF6DR14	974255	58	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	244.21	297	1097
			blastx.2	(AF128625) CDC42- binding protein kinase beta [Homo sapiens]	gb AAD37506.1 AF1 28625_1	98%	72	1733
						22%	1572	1706
HFPER82	1152249	59	blastx.14	(AC004877) sco-spondin- mucin-like; similar to P98167 1 sapiens]	gi 3638957 gb AAC3 6301.1	68%	137	90
						34%	227	123
						42%	569	513
						50%	387	346
						34%	332	255
						54%	84	52
HFPER82	909835	482	HMMER 1.8	PFAM: Protein kinase C terminal domain	PF00433	33.87	943	1047
			blastx.2	human protein kinase B [Homo sapiens]	emb CAA43372.1	89%	943	1053
HAAAO58	1091088	60	blastx.14	(AF097887) Chp [Rattus	gi 3806122 gb AAC6	100%	75	260

HAAAO58	912622	483	HMMER 2.1.1 blastx.2	norvegicus] PFAM: Ras family	9198.1] PF00071	85.9	75	365
HADFK69	1091937	61	blastx.14	(AF097887) Chp [Rattus norvegicus]	gb AAC69198.1	98%	75	467
HADFK69	912850	484	HMMER 1.8 blastx.2	(AF229839) kappa B-ras 1 [Homo sapiens] PFAM: Ras family (contains ATP/GTP binding P-loop)	gi 7008402 gb AAF34 998.1 PF00071	91%	207	752
HDPMO62	1152329	62	blastx.14	(AF229839) kappa B-ras 1 [Homo sapiens] rab-related GTP-binding protein [Homo sapiens]	gb AAF34998.1 gi 1491714 emb CAA 68227.1	90%	49	543
HDPMO62	912722	485	HMMER 1.8 blastx.2	PFAM: Ras family (contains ATP/GTP binding P-loop) rab-related GTP-binding protein [Homo sapiens]	PF00071	132.39	127	432
HDPMO85	912837	486	HMMER 1.8 blastx.2	PFAM: Ras family (contains ATP/GTP binding P-loop) (AF229840) kappa B-ras 2 [Homo sapiens] PFAM: Ras family	emb CAA68227.1 PF00071	54% 57%	133 20	444 76
HDPUY72	966153	487	HMMER 2.1.1 blastx.2	(AF112206) ras-related protein rab-14 [Homo sapiens] GTP-binding protein	gb AAF34999.1 PF00071	75.28	162	668
HDTJF87	1154640	65	blastx.14	GTP-binding protein	gb AAF34999.1 PF00071	92%	147	719
						325.7	815	207
						100%	851	219
						96%	99	254

HDTJF87	907527	488	HMMER 2.1.1 blastx.2	[Volvox carteri] PFAM: Ras family	253.1 PF00071	198.2	110	394
HE8TB94	1178794	66	blastx.14	strong similarity to the YPT1 sub-family of RAS proteins [Caenorhabditis elegans]	gb AAB52431.1	97% 73%	89 396	394 737
HE8TB94	935935	489	HMMER 2.1.1 blastx.2	ras-like protein [Homo sapiens] PFAM: Ras family	gi 190881 gb AAA36 547.1 PF00071	78% 78% 236.3	527 507 529	1075 548 1104
HE8UB55	912932	490	HMMER 1.8 blastx.2	ras-like protein [Homo sapiens] PFAM: Ras family (contains ATP/GTP binding P-loop)	gb AAA36547.1 PF00071	80% 271.56	523 197	1101 676
HEBGA65	1178633	68	blastx.14	(AL049685) hypothetical protein [Homo sapiens]	emb CAB41256.1	89%	185	688
HEBGA65	912815	491	HMMER 1.8 blastx.2	Rab24 protein [Mus musculus] PFAM: Ras family (contains ATP/GTP binding P-loop)	gi 438164 emb CAA8 0472.1 PF00071	90% 94% 176.38	435 1076 451	860 1252 939
HEGBB59	1197907	69	blastx.14	Rab24 protein [Mus musculus] RAS-LIKE PROTEIN RASD (TRANSFORMING PROTEIN P23).	emb CAA80472.1 sp P03967 RASD_DI CDI	92% 47% 57% 53%	442 671 497 944	1035 928 679 988
HEGBB59	912601	492	HMMER 1.8	PFAM: Ras family (contains ATP/GTP)	PF00071	75.96	370	546

					binding P-loop)						
					blastx.2	blastx.2	ras protein [Suberites domuncula]	emb CAA77070.1	53%	364	594
HELHC48	956003	70			HMMER 1.8	HMMER 1.8	PFAM: Ras family (contains ATP/GTP binding P-loop)	PF00071	156.24	756	403
					blastx.2	blastx.2	(AF106681) ras-related GTP-binding protein [Homo sapiens]	gb AAD43034.1	96% 76%	756 817	403 767
HEOQH90	1212646	71			blastx.14	blastx.14	GTPase Rab37.	sp AAF67162 AAF67162	93%	12	680
HEOQH90	907532	493			HMMER 1.8	HMMER 1.8	PFAM: Ras family (contains ATP/GTP binding P-loop)	PF00071	305.73	88	666
					blastx.2	blastx.2	(AB027137) RAB-26 [Homo sapiens]	dbj BAA84707.1	72%	94	657
HFKHA18	1152242	72			blastx.14	blastx.14	(AF058807) GTP-binding protein rah [Bos taurus]	gi 4587775 gb AAD25874.1	97% 95%	94 427	426 690
HFKHA18	972414	494			HMMER 1.8	HMMER 1.8	PFAM: Ras family (contains ATP/GTP binding P-loop)	PF00071	142.21	91	408
					blastx.2	blastx.2	(AF058807) GTP-binding protein rah [Bos taurus]	gb AAD25874.1	97% 93%	88 409	420 684
HFKMA10	964258	73			HMMER 1.8	HMMER 1.8	PFAM: Ras family (contains ATP/GTP binding P-loop)	PF00071	254.6	254	721
					blastx.2	blastx.2	Rab22a protein [Canis familiaris]	emb CAA80473.1	99%	242	724
HHBFM91	1092116	74			blastx.14	blastx.14	(AF091035) GTP-binding protein RAB21 [Homo sapiens]	gi 6002585 gb AAF00048.1 AF091035_1	100%	3	479

HHBFM91	912832	495	HMMER 1.8	PFAM: Ras family (contains ATP/GTP binding P-loop)	PF00071	86.13	2	340
			blastx.2	(AF091035) GTP-binding protein RAB21 [Homo sapiens]	gb AAF00048.1 AF0 91035_1	97%	2	316
HIBBF63	912715	75	HMMER 2.1.1	PFAM: Ras family	PF00071	211.1	3	416
			blastx.2	(AB027137) RAB-26 [Homo sapiens]	dbj BAA84707.1	100%	3	419
HMCEI38	1134410	76	blastx.14	(AF081353) GTP-binding protein [Homo sapiens]	gi 3859936 gb AAC7 2918.1	81%	229	594
HMCEI38	912580	496	HMMER 2.1.1	PFAM: Ras family	PF00071	103.6	297	452
			blastx.2	(AF081353) GTP-binding protein [Homo sapiens]	gb AAC72918.1	81%	228	593
HMWJD68	1154790	77	blastx.14	(AK00254) unnamed protein product [Homo sapiens]	gi 7020212 dbj BAA9 1034.1	98%	54	614
HMWJD68	912628	497	HMMER 2.1.1	PFAM: Ras family	PF00071	231.3	113	685
			blastx.2	(AK00254) unnamed protein product [Homo sapiens]	dbj BAA91034.1	99%	53	613
HOEOL58	1078090	78	blastx.14	small GTP-binding protein Rab27b [Homo sapiens]	gi 5107835 gb AAC5 1194.2	100%	102	338
HOEOL58	912836	498	HMMER 1.8	PFAM: Ras family (contains ATP/GTP binding P-loop)	PF00071	150.75	3	407
			blastx.2	small GTP-binding	gb AAC51194.2	97%	3	407

HRACA51	1162856	79	blastx.14	protein Rab27b [Homo sapiens] rab4b [Canis familiaris]	gi 919 emb CAA39800.1	100%	54	677
HRACA51	912776	499	HMMER 2.1.1 blastx.2	PFAM: Ras family	PF00071	310.6	55	666
HSHAV32	912812	500	HMMER 1.8 blastx.2	rab4b [Canis familiaris] PFAM: Ras family (contains ATP/GTP binding P-loop)	emb CAA39800.1 PF00071	100% 242.77	43 192	666 872
HTPDE66	971281	81	blastx.2 HMMER 1.8 blastx.2	(AB034244) RAB23 protein [Homo sapiens] PFAM: Ras family (contains ATP/GTP binding P-loop) small GTP-binding protein [Oryctolagus cuniculus]	dbj BAA87324.1 PF00071 gb AAA31261.1	99% 73.53 100% 63%	162 260 260 216	872 427 427 281
HTPDV73	997659	82	blastx.14	N-methyl-D-aspartate receptor subunit [Rattus rattus]	gi 286238 dbj BAA02500.1	66% 30% 70% 71% 83% 85% 71%	39 123 5 290 123 248 331	74 182 34 310 140 268 351
HTPDV73	912947	501	HMMER 1.8 blastx.2	PFAM: Ras family (contains ATP/GTP binding P-loop) (AL049685) hypothetical protein [Homo sapiens]	PF00071 emb CAB41256.1	205.32 97%	306 312	740 746
HTPHE33	963658	502	HMMER	PFAM: Ras family	PF00071	94.19	993	1433

			1.8	(contains ATP/GTP binding P-loop)				
			blastx.2	(AF095350) RAB-like protein 2A [Homo sapiens]	gb AAD51377.1 AF095350.1	83%	993	1478
HUFDN58	1224609	84	blastx.14	RAS-LIKE PROTEIN RASD (TRANSFORMING PROTEIN P23).	sp P03967 RASD_DI CDI	47%	664	921
						57%	490	672
						53%	937	981
HUFDN58	912929	503	HMMER 2.1.1	PFAM: Ras family	PF00071	80.7	42	296
			blastx.2	ras-related protein [Dictyostelium discoideum]	emb CAA78508.1	43%	3	299
HUVFX92	1225329	85	blastx.14	GTP-binding protein ypt1 [similarity] - Neurospora crassa	pir S30096 S30096	88%	54	308
HUVFX92	912672	504	HMMER 2.1.1	PFAM: Ras family	PF00071	161	81	278
			blastx.2	(AF101310) similar to RAS-related proteins; contains similarity 1	gb AAC69218.1	100%	54	275
HWAEG71	1182321	86	blastx.14	rab-related GTP-binding protein [Rattus norvegicus]	gi 206543 gb AAA42000.1	96%	85	690
HWAEG71	931547	505	HMMER 1.8	PFAM: Ras family (contains ATP/GTP binding P-loop)	PF00071	147.95	116	475
			blastx.2	rab-related GTP-binding protein [Rattus norvegicus]	gb AAA42000.1	98%	86	493
						80%	477	569

HWAHD49	1228064	87	blastx.14	GTP-BINDING PROTEIN RAH (FRAGMENT).	sp Q9XS71 Q9XS71	97% 94%	391 742	747 1011
HWAHD49	972413	506	HMMER 1.8	PFAM: Ras family (contains ATP/GTP binding P-loop)	PF00071	143.42	394	717
			blastx.2	LMW G-protein=low- molecular-weight GTP- binding protein [mice, HT4 neural cell line, Peptide, 208 aa] [Mus sp.]	gb AAB20669.1	95% 76%	391 726	720 764
HWLGG31	1178825	88	blastx.14	RAB15 [Rattus norvegicus]	gj 206537 gb AAA41 995.1	92%	81	716
HWLGG31	912581	507	HMMER 2.1.1	PFAM: Ras family	PF00071	301.8	98	562
			blastx.2	RAB15 [Rattus norvegicus]	gb AAA41995.1	90%	71	562
HWLKF25	912842	508	HMMER 2.1.1	PFAM: Ras family	PF00071	298.2	311	889
			blastx.2	(AB036693) RAB9-like protein [Homo sapiens]	dbj BAA89542.1	100%	287	889
H2CBH45	963811	90	HMMER 1.8	PFAM: Src homology domain 3	PF00018	13	194	310
			blastx.2	Kryn [Mus musculus]	dbj BAA19686.1	85% 79% 87% 70%	2 381 460 131	373 467 483 160
HAGDN53	895963	509	HMMER 1.8	PFAM: Src homology domain 3	PF00018	22.95	270	335
			blastx.2	coded for by C. elegans cDNA yk34a9.5; coded	gb AAA96115.1	43% 38%	165 103	455 156

				for by C. elegans 1 elegans]								
HAMFM39	971347	92	HMMER 1.8	PFAM: Src homology domain 3	PF00018	67.14	1136	1306				
			blastx.2	(AK001509) unnamed protein product [Homo sapiens]	dbj BAA91729.1	59%	4511	4017				
HBGQT03	908173	93	HMMER 2.1.1	PFAM: SH3 domain	PF00018	68.5	615	785				
			blastx.2	(AF130979) SH3 domain- containing protein 6511 [Homo sapiens]	gb AAF04472.1 AF1 30979_1	93%	3	791				
HBGJ13	1150790	94	blastx.14	ferrienterobactin receptor precursor [Escherichia coli]	gi 1778500 gb AAB4 0783.1	93%	729	1				
HBGJ13	878322	510	HMMER 1.8	PFAM: Src homology domain 3	PF00018	4.07	445	510				
			blastx.2	ferrienterobactin receptor precursor [Escherichia coli]	gb AAB40783.1	92%	64	684				
HBIBQ89	909782	95	HMMER 2.1.1	PFAM: SH3 domain	PF00018	49.7	212	376				
			blastx.2	p115 [Homo sapiens]	emb CAA55394.1	41%	14	397				
HCECM90	945088	96	HMMER 1.8	PFAM: Src homology domain 3	PF00018	53.06	392	568				
HCEPH71	522739	97	HMMER 1.8	PFAM: Src homology domain 3	PF00018	4.22	33	62				
HCFMT57	1175204	98	blastx.14	(AF039571) peripheral benzodiazepine receptor interacting protein; PBR- IP/PRAX1 [Homo	gi 4104812 gb AAD1 1957.1	96% 74% 100% 52%	45 702 887 381	629 887 979 500				

					sapiens]				44%	381	461
									55%	327	386
									28%	161	319
									50%	744	803
									58%	780	830
									35%	160	243
									34%	1693	1770
									47%	468	518
									55%	190	243
									58%	795	830
									42%	622	684
									29%	73	153
									42%	607	663
									35%	54	137
									36%	643	717
									31%	631	717
									25%	136	231
									38%	111	188
									28%	114	230
									28%	144	227
HCFMT57	765375	511	HMMER 1.8	PFAM: Src homology domain 3		PF00018		14.55	107	3	
			blastx.2	(AF039571) peripheral benzodiazepine receptor interacting protein; PBR- IP/PRAX1 [Homo sapiens]		gb AAD11957.1		96%	377	3	
HCOMM05	1173146	99	blastx.14	epidermal growth factor receptor kinase substrate [Homo sapiens]		gi 530823 gb AAA62 280.1		44%	456	722	
								59%	189	371	
								46%	723	851	
								23%	54	233	
								36%	126	191	

HCOMM05	925952	512	HMMER 1.8 blastx.2	PFAM: Src homology domain 3 epidermal growth factor receptor kinase substrate [Homo sapiens]	PF00018	63%	1081	1113
					gb AAA62280.1	46% 43% 23%	445 115 43	840 435 222
HCOOZ11	965306	100	HMMER 1.8 blastx.2	PFAM: Src homology domain 3 (AL022238) dJ1042K10.2 (supported by GENSCAN, FGENES and GENEWISE) [Homo sapiens]	PF00018	5.22	179	214
					emb CAA18266.1	100%	182	589
HCWFF88	506577	101	HMMER 1.8	PFAM: Src homology domain 3	PF00018	4.92	140	181
HDMAV01	911386	513	HMMER 1.8 blastx.2	PFAM: Src homology domain 3 unnamed protein product [unidentified]	PF00018	52.13	264	413
					emb CAB42388.1	73% 100%	111 3	410 116
HDPDA47	929193	103	HMMER 1.8 blastx.2	PFAM: Src homology domain 3 (AL049683) hypothetical protein [Homo sapiens]	PF00018	12.52	691	810
					emb CAB41255.1	69% 53%	145 945	1026 1022
HDPFF24	909232	104	HMMER 2.1.1 blastx.2	PFAM: KRAB box (AC007228) R31665_2 [AA 1- 673] [Homo sapiens]	PF01352	121.3	158	349
					gb AAD23606.1 AC0 07228_1	50%	158	457
HDPPO35	966248	105	HMMER 1.8 blastx.2	PFAM: Src homology domain 3 (AL049683) hypothetical	PF00018	14.07	600	749
					emb CAB41255.1	39%	84	1148

HDPSR74	911396	106	HMMER 1.8 blastx.2	protein [Homo sapiens] PFAM: Src homology domain 3 (AF104246) enhancer of filamentation 1 homolog [Gallus gallus]	PF00018	47.19	293	460
HDTKQ14	886936	107	HMMER 1.8 blastx.2	PFAM: Src homology domain 3 (AL049683) hypothetical protein [Homo sapiens]	PF00018	12.87	430	546
HE6GF02	1150897	108	blastx.14	(AJ007012) Fish protein [Mus musculus]	emb CAB41255.1 gi 3702174 emb CAA 07416.1	100% 56% 75% 66% 70% 39% 40% 38% 39% 41% 38% 37% 37% 50% 54%	439 76 795 603 189 603 804 792 795 600 582 552 150 532 459	555 291 613 427 70 430 613 637 637 427 433 481 70 485 427
HE6GF02	911263	514	HMMER 1.8 blastx.2	PFAM: Src homology domain 3 (AJ007012) Fish protein [Mus musculus]	PF00018	51.15	10	174
HE8PK12	909884	109	HMMER 1.8 blastx.2	PFAM: Src homology domain 3 (AF136380) SH3P12 protein [Homo sapiens]	emb CAA07416.1 PF00018	77% 44% 58.12	10 201 197	186 275 361
HE9SE62	911476	110	HMMER	PFAM: Src homology	gb AAD27647.1 AF1 36380_1 PF00018	82% 47.65	59 268	367 435

[illegible]

			1.8	domain 3 (AK000579) unnamed protein product [Homo sapiens]	dbj BAA91269.1	98%	252	458
HLWFN63	908437	118	HMMER 1.8	PFAM: Src homology domain 3	PF00018	12.81	515	664
			blastx.2	(AL049683) hypothetical protein [Homo sapiens]	emb CAB41255.1	44%	464	1024
HMEFT66	856149	119	HMMER 1.8	PFAM: Src homology domain 3	PF00018	28.51	5	136
HMSCD15	918133	120	HMMER 1.8	PFAM: Src homology domain 3	PF00018	41.06	453	599
			blastx.2	(AK000975) unnamed protein product [Homo sapiens]	dbj BAA91451.1	98% 29% 28%	453 387 80	635 479 175
HMSHO64	746582	121	HMMER 1.8	PFAM: Src homology domain 3	PF00018	11.08	316	405
			blastx.2	(AF030131) Plenty of SH3s; POSH [Mus musculus]	gb AAC40070.1	47%	1	411
HMTAW83	911385	122	HMMER 1.8	PFAM: Src homology domain 3	PF00018	76.18	1	159
			blastx.2	(AF230904) c-Cbl-interacting protein [Homo sapiens]	gb AAF37854.1 AF230904_1	94% 52% 48% 61% 75%	1 7 7 298 425	354 210 168 351 460
HMOVAM09	963814	123	HMMER 1.8	PFAM: Src homology domain 3	PF00018	4.79	728	802
			blastx.2	(AK001580) unnamed protein product [Homo sapiens]	dbj BAA91769.1	96%	20	802

HNSAA28	946988	124	HMMER 2.1.1 blastx.2	sapiens] PFAM: SH3 domain	PF00018	149	757	915
				(AF146277) adapter protein CMS [Homo sapiens]	gb AAD34595.1 AF1 46277_1	82%	4	1554
HNSAA28	972348	516	blastx.14	(AF146277) adapter protein CMS [Homo sapiens]	gi 4960047 gb AAD3 4595.1 AF146277_1	88%	21	449
HOGSEQ43	935465	517	HMMER 1.8 blastx.2	PFAM: Src homology domain 3	PF00018	28.13	58	132
				(AF132480) Ese2 protein [Mus musculus]	gb AAD19748.1	93%	37	132
HOUDH19	1150918	126	blastx.14	(AC007842) BC331191_1 [Homo sapiens]	gi 5080758 gb AAD3 9268.1 AC007842_3	91%	350	27
HOUDH19	908588	518	HMMER 2.1.1 blastx.2	PFAM: KRAB box	PF01352	169.7	241	429
				(AC007842) BC331191_1 [Homo sapiens]	gb AAD39268.1 AC0 07842_3	91%	226	549
HOUFT36	911293	127	HMMER 2.1.1 blastx.2	PFAM: PDZ domain (Also known as DHR or GLGF).	PF00595	35.3	322	558
				(AF162130) MAGUK protein TEM-61 [Homo sapiens]	gb AAD45919.2 AF1 62130_1	91% 98%	196 23	846 193
HPMFL08	959569	128	HMMER 1.8 blastx.2	PFAM: Src homology domain 3	PF00018	4.97	209	238
HRSMD49	723025	129	HMMER 1.8 blastx.2	PFAM: Src homology domain 3	PF00018	4.76	199	270
HSDII69	917180	130	HMMER 1.8 blastx.2	PFAM: Src homology domain 3	PF00018	4.09	382	429

HSDSB06	949151	131	HMMER 2.1.1 blastx.2	PFAM: SH3 domain (AL133047) hypothetical protein [Homo sapiens]	PF00018 emb CAB61374.1	249.3 98% 30% 33%	483 3 6 222	647 863 848 848
HSFAM09	573345	519	HMMER 1.8	PFAM: Src homology domain 3	PF00018	5.33	195	218
HSSAX53	507509	133	HMMER 1.8	PFAM: Src homology domain 3	PF00018	4.36	266	331
HSVAW49	689674	520	HMMER 1.8 blastx.2	PFAM: Src homology domain 3 (AF146277) adapter protein CMS [Homo sapiens]	PF00018 gb AAD34595.1 AF1 46277_1	36.33 97%	77 65	169 166
HTEAG49	954614	135	HMMER 1.8	PFAM: Src homology domain 3	PF00018	4.51	312	238
HTLBH67	751985	136	HMMER 1.8	PFAM: Src homology domain 3	PF00018	37.78	16	162
HTLJC71	922923	137	HMMER 1.8 blastx.2	PFAM: Src homology domain 3 (AL133030) hypothetical protein [Homo sapiens]	PF00018 emb CAB61362.1	9.14 94%	1152 3	1340 1355
HTPAD46	503313	138	HMMER 1.8	PFAM: Src homology domain 3	PF00018	4.14	160	186
HTTKP07	911390	139	HMMER 1.8 blastx.2	PFAM: Src homology domain 3 (AL049683) hypothetical protein [Homo sapiens]	PF00018 emb CAB41255.1	15.82 51% 56%	47 8 292	196 289 450
HUCOW17	933357	140	HMMER 1.8 blastx.2	PFAM: Src homology domain 3 Graf protein [Homo]	PF00018 emb CAA71414.2	20.28 67%	647 1	739 261

HWHGF52	726102	141	HMMER 1.8 blastx.2	sapiens] PFAM: Src homology domain 3 Dbs=Dbl guanine nucleotide exchange factor homolog [mice, 32D 1	PF00018 gb AAB33461.1	50% 83% 40%	608 756 187	751 809 246
HWHHB69	690442	521	HMMER 1.8 blastx.2	PFAM: Src homology domain 3 (AF178432) SH3 protein [Homo sapiens]	PF00018 gb AAF35985.1 AF1 78432 1	31.65 70% 100%	91 91 303	255 315 329
HWLFH94	1151387	143	blastx.14	(AK000265) unnamed protein product [Homo sapiens]	gi 7020230 dbj BAA9 1041.1	41% 53% 52%	545 689 949	345 594 887
HWLFH94	909682	522	HMMER 1.8 blastx.2	PFAM: Src homology domain 3 (AK000265) unnamed protein product [Homo sapiens]	PF00018 dbj BAA91041.1	58.42 40%	308 215	463 535
HWMBM13	909683	144	HMMER 1.8 blastx.2	PFAM: Src homology domain 3 Eps8 [Mus musculus]	PF00018 gb AAAI6358.1	59.64 35% 37%	126 33 324	281 317 527
HWWDN34	911357	145	HMMER 1.8 blastx.2	PFAM: Src homology domain 3 (AF053130) unconventional myosin MYO15 [Mus musculus]	PF00018 gb AAC40124.1	14.09 42% 66%	686 56 788	853 874 868
HCML27	771667	523	HMMER	PFAM: Src homology	PF00017	42.63	14	202

HELHJ69	1128924	147	1.8 blastx.2	domain 2 (AL049924) hypothetical protein [Homo sapiens]	emb CAB43208.1	88%	2	322
			blastx.14	(AF124251) SH2-containing protein Nsp3 [Homo sapiens]	gi 4704739 gb AAD28246.1 AF124251_1	81% 76% 52% 60% 63%	66 586 590 55 612	593 624 640 99 644
HELHJ69	911262	524	HMMER 1.8	PFAM: Src homology domain 2	PF00017	72.59	241	483
			blastx.2	(AF124251) SH2-containing protein Nsp3 [Homo sapiens]	gb AAD28246.1 AF124251_1	78% 76% 60%	67 587 56	645 625 100
HFKLA09	952634	525	HMMER 2.1.1	PFAM: Src homology domain 2	PF00017	46.9	758	1036
HSBBF79	965764	149	HMMER 1.8	PFAM: Src homology domain 2	PF00017	69.47	384	614
HSLKA77	911589	526	HMMER 1.8	PFAM: Src homology domain 2	PF00017	37.25	301	405
			blastx.2	tensin [Gallus gallus]	gb AAA49087.1	58% 51% 31%	178 29 3	432 115 155
hagdr21	1090433	151	blastx.14	p66shc [Homo sapiens]	gi 1899055 gb AAB49972.1	69% 72% 59% 37% 35% 34%	848 134 380 665 72 701	1150 412 475 751 164 778
hagdr21	1002124	527	blastx.14	MUS p66 Shc [Mus musculus]	gi 1200456 gb AAA91777.1	91%	62	268
HHFNH27	1025277	152	blastx.2	collagen alpha 1(III) chain	pir S05272 CGHU7L	30%	89	1609

[illegible]

					protein product [Homo sapiens]	1505.1			
HAPNV33	1151374	154	blastx.14		(AK001267) unnamed protein product [Homo sapiens]	gi 7022415 dbj BAA91590.1	100%	1	774
HAPNV33	947872	529	HMMER 1.8		PFAM: ATPases associated with various cellular activities (AAA)	PF00004	120.31	61	450
			blastx.14		(AF016427) Contains similarity to Pfam domain: 1 elegans]	gi 2291232 gb AAB65351.1	53%	1	447
HBTA84	1128800	155	blastx.14		ATP-dependent Clp protease ATP-binding subunit ClpA. [Escherichia coli]	gi 1651401 dbj BAA35601.1	100%	3	299
HBTA84	781946	530	HMMER 1.8		PFAM: ATPases associated with various cellular activities (AAA)	PF00004	20.81	122	232
HDPVY89	827026	156	HMMER 2.1.1		PFAM: ATPases associated with various cellular activities (AAA)	PF00004	30.6	431	490
HGLDB21	455474	531	HMMER 1.8		PFAM: ATPases associated with various cellular activities (AAA)	PF00004	19.89	12	80
HMIAN37	947881	158	HMMER 2.1.1		PFAM: ATPases associated with various cellular activities (AAA)	PF00004	109	436	642
			blastx.2		Similarity to Yeast MSP1 protein (TAT-binding homolog 4) (SW:MSP1_YEAST) [Caenorhabditis elegans]	emb CAA93516.1	45%	91	642

HODAK55	745532	532	HMMER 1.8	PFAM: ATPases associated with various cellular activities (AAA)	PF00004	60.69	11	157
HSLEI59	1128801	160	blastx.14	ATP-dependent Clp protease ATP-binding subunit ClpA. [Escherichia coli]	gi 1651401 dbj BAA3 5601.1	94%	3	770
HSLEI59	781945	533	HMMER 1.8	PFAM: ATPases associated with various cellular activities (AAA)	PF00004	20.14	96	206
HSQFH29	1217061	161	blastx.14	SPAF.	sp Q9Z2K7 Q9Z2K7	89% 52% 36%	101 5 854	1723 208 961
HSQFH29	967708	534	HMMER 1.8	PFAM: ATPases associated with various cellular activities (AAA)	PF00004	97.36	193	393
HTLEA35	1107230	162	blastx.14	(AF049099) SPAF [Mus musculus]	gi 4105619 gb AAD0 2481.1	83% 43% 76% 61%	70 76 408 3	417 414 470 41
HTLEA35	827028	535	HMMER 1.8	(AK001571) unnamed protein product [Homo sapiens]	gi 7022907 dbj BAA9 1764.1	100%	3	479
HUVGG63	969432	536	HMMER 1.8	PFAM: ATPases associated with various cellular activities (AAA)	PF00004	332.15	621	1178
HAGAX57	1150865	164	blastx.14	(AF159063) SKD1- homolog [Homo sapiens]	gi 5732691 gb AAD4 9227.1 AF159063_1	97%	138	1448
HAGAX57	1150865	164	blastx.14	(AF176012) J domain	gi 5815353 gb AAD5	100%	192	785

				containing protein 1 isoform a [Homo sapiens]	2650.1 AF176012_1			
HAGAX57	949211	537	HMMER 1.8 blastx.14	PFAM: DnaJ, prokaryotic heat shock protein (AF176012) J domain containing protein 1 isoform a [Homo sapiens]	PF00226 gi 5815353 gb AAD5 2650.1 AF176012_1	67.6 100%	224 185	421 778
HAMGX15	1177932	165	blastx.14	(AL032657) predicted using Genefinder; similar to 111 ES	gi 3881075 emb CAA 21734.1	64% 52% 66% 32% 45% 26%	335 560 665 623 674 626	565 667 736 733 733 751
HAMGX15	908840	538	HMMER 2.1.1 blastx.14	PFAM: DnaJ domain (AL032657) predicted using Genefinder; similar to 111 ES	PF00226 gi 3881075 emb CAA 21734.1	80.1 51%	554 506	709 715
HAUBV06	1106041	166	blastx.14	similar to [SwissProt Accession Number P08409]; 1	gi 1799806 dbj BAA1 6264.1	98% 80%	1164 2104	2120 2166
HAUBV06	596802	539	HMMER 2.1.1	PFAM: DnaJ C terminal region	PF01556	262.1	567	932
HAUBV06	929762	540	HMMER 2.1.1	PFAM: DnaJ C terminal region	PF01556	249.7	1650	1285
HBWCM62	908818	541	HMMER 1.8 blastx.14	PFAM: DnaJ, prokaryotic heat shock protein contains strong similarity to a DNAJ-like domain (PS:PS00636) [Caenorhabditis elegans]	PF00226 gi 1707079 gb AAB3 7835.1	97.9 42%	37 19	243 306

HCWFA35	1105672	168	blastx.14	Curved DNA-binding protein cbpA [Escherichia coli]	gi 1651491 dbj BAA36142.1	98%	68	322
HCWFA35	908820	542	HMMER 1.8	PFAM: DnaJ, prokaryotic heat shock protein	PF00226	116.61	80	274
			blastx.14	Curved DNA-binding protein cbpA [Escherichia coli]	gi 1651491 dbj BAA36142.1	98%	68	364
HDACA35	1107236	169	blastx.14	(AK001496) unnamed protein product [Homo sapiens]	gi 7022789 dbj BAA91724.1	76%	71	904
HDACA35	908837	543	HMMER 1.8	PFAM: DnaJ, prokaryotic heat shock protein	PF00226	65.68	68	229
			blastx.14	cysteine string protein [Bos taurus]	gi 1232165 emb CAA63355.1	49%	80	256
HDQGM08	1151469	170	blastx.14	(AF176013) J domain containing protein 1 isoform b [Homo sapiens]	gi 5815355 gb AAD52651.1 AF176013_1	100%	37	357
HDQGM08	949210	544	HMMER 1.8	PFAM: DnaJ, prokaryotic heat shock protein	PF00226	68.48	466	269
			blastx.14	(AF176013) J domain containing protein 1 isoform b [Homo sapiens]	gi 5815355 gb AAD52651.1 AF176013_1	100%	505	185
HELGB06	1148741	171	blastx.14	ORF-1 [Escherichia coli]	gi 402674 gb AAA18299.1	100%	248	3
HELGB06	935730	545	HMMER 2.1.1	PFAM: DnaJ domain	PF00226	78.3	203	421
			blastx.14	ORF-1 [Escherichia coli]	gi 402674 gb AAA18299.1	100%	200	445
HEOPR74	908836	546	HMMER 1.8	PFAM: DnaJ, prokaryotic heat shock protein	PF00226	88.67	65	262

HIBEK35	731480	173	blastx.14	cysteine string protein [Bos taurus]	gi 1232163 emb CAA 63354.1	41%	68	289
			HMMER 2.1.1	PFAM: DnaJ domain	PF00226	50%	457	492
HJMAR88	908839	547	HMMER 2.1.1	PFAM: DnaJ domain	PF00226	112.7	237	404
			blastx.14	cysteine string protein 1 - human	pir S70515 S70515	68%	6	254
			HMMER 2.1.1	PFAM: DnaJ domain	PF00226	100%	1	60
HMWGU56	908825	548	HMMER 2.1.1	PFAM: DnaJ domain	PF00226	126.9	375	569
			blastx.14	Similarity to B.subtilis DNAJ protein 1 [Caenorhabditis elegans]	gi 3873707 emb CAA 97416.1	59%	327	587
						65%	630	698
HOUDS09	1164010	176	blastx.14	(AK000034) unnamed protein product [Homo sapiens]	gi 7019854 dbj BAA9 0896.1	34%	51	200
						66%	240	659
						35%	729	1118
						45%	96	167
						32%	174	248
HOUDS09	949051	549	HMMER 1.8	PFAM: DnaJ, prokaryotic heat shock protein	PF00226	98.53	310	504
			blastx.2	(AK000034) unnamed protein product [Homo sapiens]	dbj BAA90896.1	53%	37	888
						55%	899	1033
						63%	2	34
HTEGM38	675087	177	HMMER 2.1.1	PFAM: DnaJ domain	PF00226	65.2	93	197
HTEKY82	908846	550	HMMER 2.1.1	PFAM: DnaJ domain	PF00226	119.6	281	475
			blastx.14	Similarity to B.subtilis DNAJ protein 1 [Caenorhabditis elegans]	gi 3873707 emb CAA 97416.1	53%	236	502
HTLCY54	1193550	179	blastx.14	MDJ6.	sp Q9QYI7 Q9QYI7	94%	239	460
						81%	796	927

HTLCY54	908832	551	HMMER 2.1.1 blastx.14	PFAM: DnaJ domain (AB014888) MRJ [Homo sapiens]	PF00226	81% 73% 119.8	484 610 245	597 699 445
HFOXK14	603245	180	HMMER 1.8	PFAM: Adenylate and Guanylate cyclase catalytic domain	PF00211	67% 78% 47% 40%	239 797 632 611	616 934 694 691
HHFFO69	837703	181	HMMER 1.8	PFAM: Adenylate and Guanylate cyclase catalytic domain	PF00211	386.54	124	708
HHFLU06	857884	182	HMMER 2.1.1	PFAM: Adenylate and Guanylate cyclase catalytic domain	PF00211	108.8	17	268
HAGBA56	732597	183	HMMER 2.1.1	PFAM: Eukaryotic protein kinase domain	PF00069	64.9	139	516
HAGGF84	911312	184	HMMER 1.8 blastx.14	PFAM: Eukaryotic protein kinase domain calmodulin-dependent protein kinase II-delta dash [Oryctolagus cuniculus]	PF00069	105.85	10	318
HAHGD33	921782	185	HMMER 1.8 blastx.14	PFAM: Eukaryotic protein kinase domain (AF145690) BeDNA.LD28657 [Drosophila melanogaster]	PF00069	83.68	4	564
					gi 3241849 dbj BAA28870.1	88% 87% 100%	10 366 320	363 413 364
					gi 5052670 gb AAD38665.1 AF145690_1	68% 56% 60% 39%	1 412 304 676	297 609 426 804

HAHIY08	962113	186	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	74.92	39	278
			blastx.14	similar to tyrosine kinase [Caenorhabditis elegans]				
								278 92 179
HBIOZ10	973131	187	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	121.1	3	365
			blastx.2	(AF003134) strong similarity to the CDC2/CDX subfamily of ser/thr protein kinases [Caenorhabditis elegans]				
					gb AAB54139.1	60%	3	305
HBKDI30	729048	188	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	42.23	1	213
HBXBW40	706115	189	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	34.01	280	423
HCEHE35	909937	190	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	30.78	210	347
			blastx.14	protein kinase PRK2 [human, DX3 B-cell myeloma cell line, Peptide, 984 aa] [Homo sapiens]				
					gi 914100 gb AAB33 346.1	66%	204	365
HCEPW85	911374	191	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	83.52	3	260
			blastx.14	predicted using Genefinder; Similarity to 1111 cDNA				
					gi 3875903 emb CAA 94127.1	87%	3	260
HCFAT25	932068	192	HMMER 2.1.1	PFAM: Eukaryotic protein kinase domain	PF00069	26.6	136	231
			blastx.14	(AF096300) HPK/GCK-				
					gi 4322936 gb AAD1	63%	91	456

HCFCF47	1139731	193	blastx.14	like kinase HGK [Homo sapiens] (AF003134) strong similarity to the CDC2/CDX 1	6137.1]	72% 25%	60 232	158 312
HCFCF47	894415	552	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF000069	89.54	20	295
HDAAV61	810305	194	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF000069	41.11	11	145
HDPKD75	810824	195	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF000069	98.74	68	433
HDPNC96	934520	196	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF000069	206.63	3	734
			blastx.14	HUMAN NDR [unidentified]	gi 2304746 emb CAA03387.1	92%	3	734
HDPSR15	969666	197	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF000069	87.19	351	626
			blastx.2	(AB026289) protein kinase SID6-1512 [Homo sapiens]	dbj BAA85045.1	95% 89%	631 240	1158 692
HDQDX20	919027	198	HMMER 2.1.1	PFAM: PX domain	PF00787	73.4	246	569
			blastx.14	serine/threonine protein kinase [Rattus norvegicus]	gi 294637 gb AAA42137.1	78% 44%	633 465	974 578
HDQHB19	895106	553	HMMER 2.1.1	PFAM: Eukaryotic protein kinase domain	PF000069	92.5	260	520
HDTBY88	934472	200	HMMER 2.1.1	PFAM: Eukaryotic protein kinase domain	PF000069	93.6	3	302
			blastx.14	p56 KKIAMRE protein kinase [Homo sapiens]	gi 1517820 gb AAC50918.1	82% 35%	3 192	170 458

HE2KZ07	909948	201	HMMER 1.8 blastx.14	PFAM: Eukaryotic protein kinase domain (AB004267) Ca2+/calmodulin- dependent protein kinase I beta 2 [Rattus norvegicus]	gi 3135197 dbj BAA2 8263.1	100%	492	509
HE8UY74	960914	202	HMMER 1.8 blastx.14	PFAM: Eukaryotic protein kinase domain (AF080119) contains similarity to protein kinase 1	gi 3600036 gb AAC3 5524.1	36.37%	114	407
HE9NO66	974353	203	HMMER 1.8 blastx.14	PFAM: Eukaryotic protein kinase domain (AB020741) NIK-related kinase [Mus musculus]	gi 6009519 dbj BAA8 4943.1	73% 94% 79%	449 2 748	817 283 990
HEMBT61	939957	204	HMMER 2.1.1 blastx.2	PFAM: Eukaryotic protein kinase domain (AD000092) hypothetical human serine-threonine protein kinase R31240_1 [Homo sapiens]	gb AAB51171.1	71%	13	441
HETLF29	909762	205	HMMER 1.8 blastx.14	PFAM: Eukaryotic protein kinase domain similar to cAMP- dependent protein kinase; cDNA EST 111	gi 3878636 emb CAA 88953.1	143.18%	6	416
HFIUE75	909758	206	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF000069	85.68%	377	664

			blastx.14	(AD000092) hypothetical human serine-threonine protein kinase R31240_1 [Homo sapiens]	gi 1905906 gb AAB51171.1	43%	362	634
HFKIT06	934019	207	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF000069	34.65	160	270
			blastx.14	p58 galactosyltransferase-associated protein kinase - human	pir A38282 A38282	51% 40%	178 74	270 118
HHEGG20	894409	208	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF000069	200.01	26	598
HHEHC53	921783	209	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF000069	58.81	507	797
			blastx.14	(AF145690) BcDNA.LD28657 [Drosophila melanogaster]	gi 5052670 gb AAD38665.1 AF145690_1	79% 70%	567 321	803 563
HHERQ79	944057	210	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF000069	83.4	133	474
			blastx.2	(AB016589) inducible IKappaB kinase [Mus musculus]	dbj BAA85154.1	90%	109	471
HISAF59	959140	211	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF000069	89.46	340	771
			blastx.14	(AC002343) Ser/Thr protein kinase isolog [Arabidopsis thaliana]	gi 2262107 gb AAB63615.1	39% 33%	460 397	768 468
HKAKM10	918685	212	HMMER 2.1.1	PFAM: Eukaryotic protein kinase domain	PF000069	31.4	8	127
HLTHP86	919354	213	HMMER 2.1.1	PFAM: TBC domain	PF00566	69.4	855	1274
			blastx.2	(AF161420) HSPC302	gb AAF28980.1 AF1	89%	456	1352

HMSJL96	934483	214	HMMER 1.8	[Homo sapiens] PFAM: Eukaryotic protein kinase domain	61420_1	99% 52%	1309 1253	1974 1309
HMTAJ73	813296	215	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF000069	26.49	199	363
HNTCP13	909770	216	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF000069	21.34	4	114
			blastx.14	PFAM: Eukaryotic protein kinase domain	PF000069	102.96	445	930
			blastx.14	(AC006530) unknown [Homo sapiens]	gi 4809337 gb AAD3 0182.1 AC006530_4	55%	463	957
HNTMD79	934522	217	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF000069	130.82	203	586
			blastx.14	LATS [Drosophila melanogaster]	gi 903942 gb AAA70 336.1	52% 33% 57% 22%	239 76 169 64	586 156 210 240
HNTMH70	757184	218	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF000069	94.55	176	577
HNTNB14	909942	219	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF000069	96.28	38	343
			blastx.14	calmodulin-binding protein [Rattus norvegicus]	gi 349075 gb AAA16 633.1	97% 85% 74% 77% 69% 65% 60% 52% 37% 39% 35% 33%	41 553 553 553 559 553 553 553 553 553 553 559	475 657 657 657 657 657 657 654 657 636 645 657

HODFF88	974911	220	HMMER 1.8 blastx.14	PFAM: Eukaryotic protein kinase domain mixed-lineage protein kinase 1 - human	PF00069 pir S32467 JU0229	77% 29% 101.43	512 556 98	538 657 370
HOHCE47	911566	554	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	79.42	211	423
HPCRV84	945856	222	HMMER 1.8 blastx.2	PFAM: Eukaryotic protein kinase domain similar to protein kinase of X.laevis, has putative 1	PF00069 dbj BAA11492.1	75.57 78%	157 127	384 483
HRACK83	888037	223	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	48.4	211	423
HRADM45	717358	224	HMMER 1.8 blastx.2	PFAM: Eukaryotic protein kinase domain (A 271722) putative serine/threonine protein kinase MAK-V [Homo sapiens]	PF00069 emb CAB71146.1	23.7 98%	14 2	124 469
HRAED74	942527	225	HMMER 1.8 blastx.2	PFAM: Eukaryotic protein kinase domain (AB023658) Ca/calmodulin-dependent protein kinase kinase alpha, CaM-kinase kinase alpha [Rattus norvegicus]	PF00069 dbj BAA75246.1	59.6 97% 81% 71% 88%	406 71 388 342 662	612 346 648 425 688
HRDZ70	942673	226	HMMER 2.1.1 blastx.2	PFAM: Eukaryotic protein kinase domain kinase like protein	PF00069 emb CAB10257.1	78.2 39%	33 33	248 323

HSKAC24	823869	227	HMMER 1.8	[Arabidopsis thaliana] PFAM: Eukaryotic protein kinase domain	PF00069	50%	303	380
HSSMT34	911294	228	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	53.16	95	292
HT3BG12	921593	229	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	27.09	109	183
			blastx.14	CYCLIN-DEPENDENT KINASE (CDK)8 [unidentified]	gi 3715669 emb CAA 03585.1	85%	1	246
HTEGO05	932583	230	HMMER 2.1.1	PFAM: Eukaryotic protein kinase domain	PF00069	50.8	3	233
			blastx.14	male germ cell-associated kinase (mak) [Rattus norvegicus]	gi 205278 gb AAA41 562.1	85% 64% 85% 38%	3 489 768 1023	395 761 848 1100
HTEKT33	953308	231	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	200.58	428	1393
			blastx.2	(AC007661) putative protein kinase [Arabidopsis thaliana]	gb AAD32787.1 AC0 07661_24	41% 36% 29%	722 1070 428	1009 1243 628
HTEMU66	944419	232	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	114.85	613	963
			blastx.2	MEK Kinase 3 [Mus musculus]	gb AAB03535.1	49% 29%	604 209	948 340
HTEMV09	909843	233	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	99.16	19	312
			blastx.14	protein kinase I [Rattus norvegicus]	gi 406113 gb AAA19 670.1	44%	1	321
HTEMV66	1151075	234	blastx.14	contains EGF-like repeats; highly similar to ZC84.1;	gi 495684 gb AAA50 735.1	55% 44%	579 783	223 649

				1					
HTMV66	813038	555	HMMER 2.1.1	PFAM: Eukaryotic protein kinase domain	PF00069		861	772	
HTGAU79	1175071	235	blastx.14	(AL157917) similarity to endopeptidases 1	gi 7106102 emb CAB 76028.1	27.8	154	315	
HTGAU79	940369	556	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	50%	755	976	
HTLEJ11	973302	236	blastx.2	(AL157917) similarity to endopeptidases [Schizosaccharomyces 1	emb CAB76028.1	38%	371	571	
HTLIY52	1218691	237	HMMER 2.1.1	PFAM: Eukaryotic protein kinase domain	PF00069	60%	641	730	
HTLIY52	942161	557	blastx.14	(AF144573) Mx- interacting protein kinase PKM [Mesocricetus auratus]	gi 4868443 gb AAD3 1319.1 AF144573_1	52%	323	373	
HTOAK34	966800	238	HMMER 1.8	TESTIS-SPECIFIC SERINE/THREONINE KINASE.	sp Q61241 Q61241	31.25	315	779	
			blastx.2	PFAM: Eukaryotic protein kinase domain	PF00069	45%	324	977	
			HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	55.9	44	223	
			blastx.14	(AF144573) Mx- interacting protein kinase PKM [Mesocricetus auratus]	gi 4868443 gb AAD3 1319.1 AF144573_1	69%	35	268	
			HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	40%	437	592	
			blastx.2	PFAM: Eukaryotic protein kinase domain	PF00069	42%	293	397	
			HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	38%	877	939	
			blastx.14	PFAM: Eukaryotic protein kinase domain	PF00069	46%	640	972	
			HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	48%	142	414	
			blastx.2	PFAM: Eukaryotic protein kinase domain	PF00069	45%	427	579	
			HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	42%	565	621	
			blastx.14	PFAM: Eukaryotic protein kinase domain	PF00069	251.19	166	933	
			HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	44%	133	936	
			blastx.2	PFAM: Eukaryotic protein kinase domain	PF00069	32.41	1020	1190	
			HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	75%	954	1190	
			blastx.14	(AF084205) serine/threonine protein kinase TAO1 [Rattus	gi 3452473 gb AAC7 1014.1				

HTPGG25	911282	239	HMMER 1.8 blastx.2	norvegicus] PFAM: Eukaryotic protein kinase domain (AL117482) hypothetical protein [Homo sapiens]	PF000069	114.02	72	353
					emb CAB55955.1	94% 92% 63%	9 350 2	353 622 58
HUJAD24	1161319	240	blastx.14	serine/threonine kinase [Rattus norvegicus]	gi 2052191 emb CAB 06295.1	34% 48% 34% 57% 48% 24% 47% 72% 42%	439 345 779 267 123 57 3 211 162	759 494 910 344 215 206 53 243 218
HUJAD24	911498	558	HMMER 1.8 blastx.14	PFAM: Eukaryotic protein kinase domain AMP-activated protein kinase homolog [Homo sapiens]	PF000069	34.73	9	215
					gi 758783 gb AAA64 850.1	45% 45% 37% 54% 41%	336 123 267 211 45	467 215 338 243 95
HUTSF11	966029	241	HMMER 1.8 blastx.14	PFAM: Eukaryotic protein kinase domain PRO1038.	PF000069	27.74	3	104
HUVGZ88	1227628	242			sp AAAF71042 AAAF71 042	59% 41% 39% 75%	425 1159 1282 1695	859 1296 1404 1742
HUVGZ88	959020	559	HMMER 1.8 blastx.14	PFAM: Eukaryotic protein kinase domain (AF191838) TANK binding kinase TBK1	PF000069	31.12	182	439
HWADY66	1096252	243			gi 6224868 gb AAAF05 989.1 AF191838.1	84%	10	183

HWADY66	734565	560	HMMER 1.8	[Homo sapiens] PFAM: Eukaryotic protein kinase domain	PF00069	28.82	1	174
HWAFG04	952878	244	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	93.74	1655	945
			blastx.14	(AC002343) Ser/Thr protein kinase isolog [Arabidopsis thaliana]	gi 2262107 gb AAB6 3615.1	41% 48% 42% 75%	1655 1319 1046 1355	1383 1185 933 1332
			HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	115.98	225	632
HWAFS18	948434	245	HMMER 1.8	(AF156884) RIP-like kinase [Homo sapiens]	gi 5059425 gb AAD3 9005.1 AF156884_1	91% 66% 100%	165 702 632	632 773 661
			blastx.14	(AF156884) RIP-like kinase [Homo sapiens]	gi 5059425 gb AAD3 9005.1 AF156884_1	82%	1	273
HWAGS73	1150212	246	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	64.17	4	273
HWLEA48	927676	247	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	32.82	190	381
			blastx.2	(AF169034) protein kinase [Homo sapiens]	gb AAF12757.2 AF1 69034_1	59% 100% 51%	154 89 287	429 166 415
			HMMER 2.1.1	PFAM: Eukaryotic protein kinase domain	PF00069	147.2	2	319
HWLHS82	934505	248	blastx.2	(AC005581) R31237_1, partial CDS [Homo sapiens]	gb AAC33487.1	90% 100% 40%	68 2 306	364 76 422
			HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	122.85	1458	934
HWMIB81	955336	249	blastx.2	(AK000528) unnamed	dbj BAA91232.1	100%	3	572

HCWDV17	1105673	250	blastx.14	protein product [Homo sapiens] BvgA positive transcription regulator (put.); putative [Bordetella pertussis]	gi 144039 gb AAA22969.1	57% 70%	203 77	604 187
HCWDV17	974478	562	HMMER 1.8	PFAM: Bacterial regulatory proteins, luxR family	PF00196	81.59	416	613
HELDI95	1103374	251	blastx.14	Regulatory protein KdpD. [Escherichia coli]	gi 1651302 dbj BAA35352.1	100%	103	525
HELDI95	953059	563	HMMER 1.8	PFAM: Response regulator receiver domain	PF00072	123.84	482	766
HAGFO25	1150845	252	blastx.14	Regulatory protein KdpD. [Escherichia coli]	gi 1651302 dbj BAA35352.1	98%	1	432
HAGFO25	957992	564	HMMER 1.8	(AF062595) adenylate kinase 5 [Homo sapiens]	gi 4691541 gb AAD27956.1 AF062595_1	92%	145	732
HAWAB54	1149319	253	blastx.14	PFAM: Adenylate kinases	PF00406	206.82	180	650
HAWAB54	957993	565	HMMER 2.1.1	(AF062595) adenylate kinase 5 [Homo sapiens]	gi 4691541 gb AAD27956.1 AF062595_1	90%	135	728
HLIBV06	934887	254	HMMER 2.1.1	(AF062595) adenylate kinase 5 [Homo sapiens]	gi 4691541 gb AAD27956.1 AF062595_1	92% 30% 29%	876 1341 1413	283 1012 1321
				PFAM: Adenylate kinase	PF00406	40.1	111	296
				(AF062595) adenylate kinase 5 [Homo sapiens]	gi 4691541 gb AAD27956.1 AF062595_1	98%	111	374
				PFAM: Adenylate kinase	PF00406	100.8	81	245
				(AB020203) adenylate	gi 4760600 dbj BAA7	90%	81	350

HMALL66	1105097	255	blastx.14	kinase isozyme 3 [Mus musculus]	7360.1				
				adenylate kinase (EC 2.7.4.3), chloroplast - maize	pir S45634 S45634	45%	71	292	
HMALL66	956195	566	HMMER 1.8	PFAM: Adenylate kinases	PF00406	50.17	63	296	
HOACE12	858976	256	HMMER 2.1.1	PFAM: Adenylate kinase	PF00406	46.1	20	235	
HOGCG69	924848	257	HMMER 1.8	PFAM: Adenylate kinases	PF00406	76.14	858	1145	
			blastx.14	adenylate kinase (EC 2.7.4.3), chloroplast - maize	pir S45634 S45634	36%	480	791	
						35%	849	1145	
						33%	379	522	
						57%	214	255	
HAGAE09	525926	567	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	3.93	159	185	
HAGAE34	525878	568	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	8.88	191	253	
HARMH78	1137572	260	blastx.14	(AF001435) unknown [Homo sapiens]	gi 2529709 gb AAB81205.1	32%	237	395	
						43%	135	203	
						75%	482	505	
HARMH78	773210	569	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	4.88	192	227	
HBILB53	974122	570	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	4.62	301	348	
HBJNB52	726475	571	HMMER	PFAM: Phorbol esters /	PF00130	3.77	193	252	

HDABQ83	669619	572	1.8	diacylglycerol binding domain	PF00130	6.04	255	284
HDPDC84	616980	573	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	25.6	253	393
HDPUF40	1212494	265	blastx.14	PTPL1-ASSOCIATED RHOGAP.	sp O15463 O15463	54% 46% 23%	286 1018 1537	867 1230 1662
HDPUF40	970586	574	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	26.42	415	546
			blastx.14	similar to C.elegans protein (Z37093) [Homo sapiens]	gi 1504026 dbj BAA13212.1	94% 98%	61 654	651 806
HDPWU07	952734	575	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	2.94	333	356
HDTJJ02	913787	576	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	5.7	21	68
HE2GA18	1121872	268	blastx.14	mhpR [Escherichia coli]	gi 1702880 emb CAA70746.1	98%	288	1
HE2GA18	867276	577	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	4.09	74	109
HE2SY03	947947	578	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	2.97	387	437

HELGY64	934511	579	blastx.14	(AF118023) SH3 domain-binding protein SNP70 [Homo sapiens]	gi 4836401 gb AAD30425.1 AF118023_1	46%	456	301
HFIYW31	697730	580	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	76.38	241	390
HFVIP88	960741	581	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	3.29	29	67
HGBAS76	771320	582	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	7.32	147	206
HHEBB62	1151481	274	blastx.14	(AK000193) unnamed protein product [Homo sapiens]	gi 7020117 dbj BAA91000.1	100%	1	375
HHEBB62	791469	583	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	6.2	292	236
HHEHU73	923895	584	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	4.1	115	156
HHEMA11	966924	585	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	10.16	354	395
HHEQK01	1107392	277	blastx.14	ORF 3 [Homo sapiens]	gi 182221 gb AAA58464.1	37% 55% 39%	165 266 342	22 213 274
HHEQK01	871911	586	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	3.27	64	90

HHPEM84	915639	278	HMMER 1.8	domain PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	12.35	146	187
HHSED84	706739	587	HMMER 2.1.1	PFAM: Sterol O- acyltransferase	PF01800	276.4	2	364
HIBCC94	504326	588	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	3.12	177	206
HKADN56	1220254	281	blastx.14	CG5276 PROTEIN.	sp Q9VGN8 Q9VGN8	58% 68% 54% 43% 63% 47% 87% 42%	904 1465 1279 796 754 706 1627 102	1257 1617 1437 891 810 756 1650 158
HKADN56	968619	590	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	5.32	207	233
HKIXG58	464241	591	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	3.59	84	137
HLICI13	626559	592	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	4.83	328	378
HLTGF17	662405	284	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	3.46	136	183
HLYDC50	1151494	285	blastx.14	similar to C.elegans protein (Z37093) [Homo sapiens]	gi 1504026 dbj BAAI 3212.1	59% 52% 37%	275 719 32	652 871 127

HL YDC50	677050	593	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	29.67	191	319
HMADD49	1217031	286	blastx.14	L-aspartate oxidase (EC 1.4.3.16) nadB [validated] -1	pir E65035 OXECLD	100%	2212	803
HMADD49	867481	594	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	3.79	131	175
HMEKE78	792383	595	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	3.04	3	35
HMSHU26	681745	596	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	6.77	158	226
HNEEB82	778884	597	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	3.33	126	152
HNHIA06	859932	598	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	3.13	123	146
HODFY16	958329	599	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	3.15	175	213
HPQSB68	740087	600	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	3.9	170	247
HRDBH04	922022	601	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	5.19	600	632
HSICR69	531061	602	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	3.1	190	213

HSIGJ94	793624	603	HMMER 1.8	domain PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	3.15	207	239
HSYBL15	1104299	296	blastx.14	(AF021935) mytonic dystrophy kinase-related Cdc42-binding kinase [Rattus norvegicus]	gi 2736151 gb AAC0 2941.1	94%	2	931
HSYBL15	660053	604	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	22.31	2	70
HTEKH29	855660	297	HMMER 2.1.1	PFAM: Phorbol esters/diacylglycerol binding domain (CI domain)	PF00130	42.4	1660	1803
HTGEL46	685425	605	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	7.26	398	433
HTGFA05	972982	606	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	4.17	905	855
HTLDU61	530316	607	blastx.2	phosphorylation regulatory protein HP-10 - human	pir A61382 A61382	99% 100% 74% 100%	214 1080 827 67	909 1259 1078 213
			HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	5.45	102	125
HTOFT34	527144	608	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	4.53	235	264
HTTDH46	1152491	302	blastx.14	F10B5.8 [Caenorhabditis]	gi 5824432 emb CAB	74%	32	607

HTTDH46	951114	609	HMMER 1.8	elegans] PFAM: Phorbol esters / diacylglycerol binding domain	54223.1 PF00130	70%	623	1144
			blastx.14	F10B5.8 [Caenorhabditis elegans]	gi 5824432 emb CAB 54223.1	73%	117	437
HTTIO05	931037	610	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	73%	2	124
						4.25	1289	1330
HWHGY45	911621	304	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	10.67	123	203
HWLQR48	914556	611	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	4.03	359	391
HWLQX76	894607	612	HMMER 2.1.1	PFAM: RhoGAP domain	PF00620	97.4	715	963
HATDD09	1165331	307	blastx.14	(AK00239) unnamed protein product [Homo sapiens]	gi 7020190 dbj BAA9 1027.1	52%	3	260
HATDD09	573794	613	HMMER 1.8	PFAM: Cyclic nucleotide- binding domain	PF00027	9.43	59	124
HBJGT03	923800	614	HMMER 1.8	PFAM: Cyclic nucleotide- binding domain	PF00027	8.96	41	100
HMTMF45	1141737	309	blastx.14	(AL109657) dJ842G6.1 (novel protein) [Homo sapiens]	gi 6691957 emb CAB 65791.1	96%	108	377
						100%	476	700
HMTMF45	553382	615	HMMER 1.8	PFAM: Cyclic nucleotide- binding domain	PF00027	8.27	230	292
HHPDV86	522953	310	HMMER 2.1.1	PFAM: PH domain	PF00169	33	196	531

HE8BT56	732602	311	HMMER 2.1.1	PFAM: Ras family	PF00071	46.1	138	248
HUJDH06	907613	312	HMMER 2.1.1	PFAM: ADP-ribosylation factor family	PF00025	62.3	433	669
			blastx.14	(AF143680) arf-like protein 2 [Mus musculus]	gi 4929218 gb AAD3 3908.1 AF143680.1	32% 48%	421 264	663 356
HOEJG61	907614	313	HMMER 2.1.1	PFAM: ADP-ribosylation factor family	PF00025	45.6	399	566
			blastx.14	(AF031903) ADP- ribosylation-like factor homolog ARL6 [Mus musculus]	gi 3687625 gb AAC6 2194.1	75% 48%	399 566	566 652
HE8PN24	907620	314	HMMER 1.8	PFAM: ADP-ribosylation factors (Arf family) (contains ATP/GTP binding P-loop)	PF00025	104.77	197	568
			blastx.14	ADP-ribosylation factor [Candida albicans]	gi 727191 gb AAA64 266.1	38% 34%	191 386	430 568
HGBHI37	909745	315	HMMER 2.1.1	PFAM: PH domain	PF00169	30.1	107	259
			blastx.14	(AF017368) faciogenital dysplasia protein 2 [Mus musculus]	gi 3599940 gb AAC3 5430.1	82% 63%	14 145	151 201
HCHOK82	909755	316	HMMER 2.1.1	PFAM: RhoGEF domain	PF00621	176.8	40	519
			blastx.14	(AF017369) faciogenital dysplasia protein 3 [Mus musculus]	gi 3599942 gb AAC3 5431.1	90% 79% 100%	31 855 1062	849 941 1082
HFPCH24	912608	317	HMMER 1.8	PFAM: Ras family (contains ATP/GTP binding P-loop)	PF00071	43.25	47	307

			blastx.14	rap2b gene product (AA 1-183) [Homo sapiens]	gi 35863 emb CAA37178.1	41%	35	229
HTTKF86	912689	318	HMMER 2.1.1	PFAM: Ras family	PF00071	29.6	98	223
HCESA79	912709	319	HMMER 2.1.1	PFAM: Ras family	PF00071	45.1	67	243
			blastx.14	(AB027137) RAB-26 [Homo sapiens]	gi 5931612 dbj BAA84707.1	92%	52	246
HDTBJ28	912714	320	HMMER 2.1.1	PFAM: Ras family	PF00071	28.1	21	137
			blastx.14	Rab12 protein [Canis familiaris]	gi 437985 emb CAA80471.1	88%	21	98
HDPBF48	912783	321	HMMER 2.1.1	PFAM: Ras family	PF00071	26.1	33	101
			blastx.14	(AL117204) predicted using Genefinder [Caenorhabditis elegans]	gi 5832782 emb CAB55120.1	48%	123	209
						55%	258	338
						68%	33	89
						53%	429	467
HTPFY55	912928	322	HMMER 2.1.1	PFAM: Ras family	PF00071	27.2	240	386
			blastx.14	similar to the RAS gene family [Caenorhabditis elegans]	gi 1572819 gb AAB09163.1	48%	117	383
						60%	396	524
HMSCM47	923632	323	HMMER 2.1.1	PFAM: ATPases associated with various cellular activities (AAA)	PF00004	121.1	65	652
			blastx.2	(AF033862) Lon protease [Arabidopsis thaliana]	gb AAC05085.1	65%	5	673
HEOQA56	925132	324	HMMER	PFAM: Ras family	PF00071	62.8	53	154

HTPCQ24	925349	325	1.8	(contains ATP/GTP binding P-loop) GTP-binding protein [Discopyge ommata] PFAM: PH domain	gi 213115 gb AAA49230.1 PF00169	76%	23	202
HWAEI37	929481	326	HMMER 2.1.1	PFAM: MCM2/3/5 family	PF00493	59.7	8	415
HDPSF03	969536	327	HMMER 2.1.1	(AL035461) dJ967N21.5 (novel MCM2/3/5 family member) [Homo sapiens] PFAM: ATPases associated with various cellular activities (AAA)	gi 5834569 emb CAB55276.1 PF00004	100% 92%	323 2	415 85
HLHST63	581528	328	HMMER 2.1.1	LON1 protease [Zea mays]	gi 1816586 gb AAC50011.1 PF00071	58% 62% 41% 36% 30%	46 865 622 580 642	447 1200 846 636 710
HFAAJ44	489201	329	HMMER 2.1.1	PFAM: Ras family	PF01694	49.5	6	299
HSLEM44	506604	330	HMMER 2.1.1	PFAM: Rhomboid family	PF00873	137.4	2	256
HETCL79	522826	331	HMMER 2.1.1	PFAM: ActB/AcrD/AcrF family PFAM: PDZ domain (Also known as DHR or GLGF)	PF00595	28.1	242	457
HFTAR20	670041	332	HMMER 2.1.1	PFAM: Glypican	PF01153	170.7	12	308
HCUFD32	699379	333	HMMER	PFAM: PDZ domain	PF00595	29.3	124	369

			2.1.1	(Also known as DHR or GLGF).				
HKAEO39	705332	334	HMMER 2.1.1	PFAM: PDZ domain (Also known as DHR or GLGF).	PF00595	25.7	239	430
HLWBR95	734474	335	HMMER 2.1.1	PFAM: PDZ domain (Also known as DHR or GLGF).	PF00595	46.8	270	434
HPWCJ63	772553	336	HMMER 2.1.1	PFAM: DedA family	PF00597	228	235	717
			blastx.2	(AE000391) orf, hypothetical protein [Escherichia coli]	gb AAC76130.1	100%	148	807
HPWCJ63	957495	618	HMMER 2.1.1	PFAM: DedA family	PF00597	228	1152	670
			blastx.2	(AE000391) orf, hypothetical protein [Escherichia coli]	gb AAC76130.1	100%	144	803
HBXCM35	782911	337	HMMER 2.1.1	PFAM: PDZ domain (Also known as DHR or GLGF).	PF00595	27.5	251	397
HULBN83	857836	338	HMMER 2.1.1	PFAM: PDZ domain (Also known as DHR or GLGF).	PF00595	38	133	363
HAGET77	885265	339	HMMER 2.1.1	PFAM: Ezrin/radixin/moesin family	PF00769	37.6	770	841
HMSOZ55	910911	340	HMMER 2.1.1	PFAM: PDZ domain (Also known as DHR or GLGF).	PF00595	66.7	276	500
			blastx.14	(AF090136) lin-7-C	gi 3885834 gb AAC7	89%	3	500

HAPOR42	911292	341	HMMER 2.1.1	[Rattus norvegicus] PFAM: PDZ domain (Also known as DHR or GLGF).	8075.1 PF00595	74%	461	589
			blastx.14	(AF061262) semaF cytoplasmic domain associated protein 2 [Mus musculus]	gi 3851518 gb AAC7 2310.1	88% 83% 80% 50%	249 679 968 1009	644 966 1012 1050
HMVAU10	911449	342	HMMER 2.1.1	PFAM: PDZ domain (Also known as DHR or GLGF).	PF00595	68.6	140	394
HTTFY29	911454	343	HMMER 2.1.1	PFAM: PDZ domain (Also known as DHR or GLGF).	PF00595	101	180	428
			blastx.14	(AF034746) LNXp70 [Mus musculus]	gi 3041881 gb AAC4 0076.1	55% 58% 34% 60% 26% 32%	150 3 258 552 255 99	467 146 422 626 413 173
HHFJY06	911456	344	HMMER 2.1.1	PFAM: PDZ domain (Also known as DHR or GLGF).	PF00595	59.7	99	326
			blastx.14	(AJ001320) multi PDZ domain protein 1 [Rattus norvegicus]	gi 2959979 emb CAA 04681.1	40% 29%	132 427	359 519
HPCIK72	911459	345	HMMER 2.1.1	PFAM: PDZ domain (Also known as DHR or GLGF).	PF00595	72	36	260
			blastx.14	neuroendocrine-dlg [Homo sapiens]	gi 1515355 gb AAB6 1453.1	58% 48% 43%	180 180 15	266 260 110

HFIDT84	919878	346	HMMER 2.1.1	PFAM: PDZ domain (Also known as DHR or GLGF).	PF00595		40%	105	179
			blastx.14	(AF034746) LNXp70 [Mus musculus]	gi 3041881 gb AAC4 0076.1		33%	21	110
							45%	36	95
							40%	114	179
							225.5	1879	2127
							88%	256	1455
							91%	1774	2151
							82%	1462	1782
							30%	1462	1728
							34%	1597	1779
							29%	1876	2121
							50%	895	1002
							25%	1183	1422
							26%	1570	1728
							57%	808	849
							50%	1504	1545
							36%	1507	1596
HMCAV88	924874	347	HMMER 2.1.1	PFAM: PDZ domain (Also known as DHR or GLGF).	PF00595		70.4	235	471
			blastx.14	(AL110228) hypothetical protein [Homo sapiens]	gi 5817167 emb CAB 53685.1		41%	232	471
							37%	574	645
HKAIPT3	928809	348	HMMER 2.1.1	PFAM: PDZ domain (Also known as DHR or GLGF).	PF00595		48.9	1041	805
			blastx.14	(AF131809) Unknown [Homo sapiens]	gi 4406642 gb AAD2 0049.1		99%	1107	487
HFVHV40	945849	349	HMMER 2.1.1	PFAM: Adaptor complexes medium subunit family	PF00928		349.2	123	680

HTJN180	952231	350	blastx.2	clathrin-associated protein [Mus musculus]	gb AAA37244.1	98%	108	680
			HMMER 2.1.1	PFAM: PDZ domain (Also known as DHR or GLGF).	PF00595	27.1	92	316
HEAAE08	959970	351	HMMER 2.1.1	PFAM: PDZ domain (Also known as DHR or GLGF).	PF00595	78.5	277	516
			blastx.14	(AF090133) lin-7-A [Rattus norvegicus]	gi 3885828 gb AAC7 8072.1	96%	223	612
HDPLU91	963199	352	HMMER 2.1.1	PFAM: GNS1/SUR4 family	PF01151	27.2	452	550
			blastx.2	(AL034374) dJ483K16.1 (novel protein) [Homo sapiens]	emb CAB41293.1	100%	305	700
HAPRM21	963200	353	HMMER 2.1.1	PFAM: GNS1/SUR4 family	PF01151	43.3	244	378
			blastx.14	(AL034374) dJ483K16.1 (novel protein) [Homo sapiens]	gi 4680391 emb CAB 41293.1	100%	1	630
HTDAB30	965320	354	HMMER 2.1.1	PFAM: Adaptor complexes medium subunit family	PF00928	493.4	81	896
H2CBN90	966919	355	HMMER 2.1.1	PFAM: PDZ domain (Also known as DHR or GLGF).	PF00595	62.4	609	821
			blastx.14	(AB005549) atypical PKC specific binding protein [Rattus norvegicus]	gi 3868778 dbj BAA3 4216.1	78%	6	821
HETFJ47	971305	356	HMMER 2.1.1	PFAM: Adaptor complexes medium	PF00928	797.6	75	1325

				blastx.14	subunit family (AF020797) AP-mu chain family member mu1B [Homo sapiens]	gi 4587714 gb AAD2 5870.1 AF020797_1	99% 100%	60 1155	950 1328
HADEX52	971351	357		HMMER 2.1.1	PFAM: PDZ domain (Also known as DHR or GLGF).	PF00595	63.3	134	388
HTADZ74	811489	358		HMMER 2.1.1	PFAM: TIR domain	PF01582	53.1	305	538
HAPNZ77	887072	359		HMMER 2.1.1	PFAM: TIR domain	PF01582	31.9	292	483
HELD74	963001	360		HMMER 2.1.1	PFAM: TIR domain	PF01582	46.5	492	779
				blastx.2	(AF113795) toll/interleukin-1 receptor 8 [Mus musculus]	gb AAF26200.1 AF1 13795_1	74%	201	1223
HDPLJ22	859915	361		HMMER 2.1.1	PFAM: Cullin family	PF00888	39.1	86	409
HPMLD11	890204	362		HMMER 2.1.1	PFAM: Scavenger receptor cysteine-rich domain	PF00530	119.6	57	350
HMVDZ78	938574	363		HMMER 2.1.1	PFAM: IPT/TIG domain	PF01833	52.6	104	244
HTSFJ40	722406	364		HMMER 2.1.1	PFAM: GTPase of unknown function	PF01926	37.5	96	356
HEMBZ62	742551	365		HMMER 2.1.1	PFAM: GTPase of unknown function	PF01926	42.4	23	175
HHFGZ38	785591	366		HMMER 2.1.1	PFAM: GTPase of unknown function	PF01926	97.2	338	799
HDPLN70	854010	367		HMMER 2.1.1	PFAM: WH1 domain	PF00568	33.1	400	573

HSDJH12	876344	368	HMMER 2.1.1	PFAM: GTPase of unknown function	PF01926	115.7	207	572
HNBUT01	913838	369	HMMER 2.1.1	PFAM: GTPase of unknown function	PF01926	149.3	30	503
			blastx.14	(AL035632) BACN32G11.d [Drosophila melanogaster]	gi 4481810 emb CAB 38462.1	71% 36%	30 768	506 824
HEOQN14	923752	370	HMMER 2.1.1	PFAM: GTPase of unknown function	PF01926	33.9	927	562
			blastx.14	(AC002510) unknown protein [Arabidopsis thaliana]	gi 2618702 gb AAB8 4349.1	54%	951	787
HTXKL86	928194	371	HMMER 2.1.1	PFAM: GTPase of unknown function	PF01926	133.3	10	636
			blastx.14	similar to hypothetical proteins [Bacillus subtilis]	gi 2633977 emb CAB 13478.1	37% 33% 54% 31% 30%	4 493 334 229 355	219 690 405 285 444
			HMMER 2.1.1	PFAM: WH1 domain	PF00568	140.5	132	458
			blastx.14	ena-VASP like protein [Mus musculus]	gi 1644453 gb AAC5 2862.1	97% 78% 91% 27% 35% 26% 38%	135 771 1215 751 1266 1035 880	539 1157 1358 879 1316 1148 933
			HMMER 2.1.1	PFAM: GTPase of unknown function	PF01926	51.1	460	624
HE8TM80	955022	373	blastx.14	similar to GTP-binding protein; cDNA EST 111	gi 3878119 emb CAA 88860.1	59% 55%	463 4	624 90

HWLEY40	957875	374	HMMER 2.1.1 blastx.14	this gene PFAM: GTPase of unknown function (AC002510) unknown protein [Arabidopsis thaliana]	PF01926	103.9	192	632
HDPPD36	964320	620	HMMER 2.1.1 blastx.14	PFAM: WH1 domain	gi 2618702 gb AAB8 4349.1	54% 50% 70%	1209 168 516	1373 347 575
HOUBZ94	527876	376	HMMER 2.1.1	PFAM: WH1 domain	PF00568	32.6	200	361
HMIAH32	550977	377	HMMER 2.1.1	AE33 protein - fruit fly (Drosophila melanogaster)	pir JC5909 JC5909	48% 80%	170 50	391 79
HDPH43	573418	378	HMMER 2.1.1	PFAM: Phosphotyrosine interaction domain (PTB/PID).	PF00640	41.1	7	129
HCE3W04	615501	379	HMMER 2.1.1	PFAM: Guanine nucleotide exchange factor for Ras-like GTPases; N-terminal motif	PF00618	28.9	253	441
HMUBZ20	670393	380	HMMER 2.1.1	PFAM: PX domain	PF00787	38.5	13	336
HDPAB51	685665	381	HMMER 2.1.1	PFAM: RhoGEF domain	PF00621	46.1	535	804
HPJAP28	686349	382	HMMER 2.1.1	PFAM: PX domain	PF00787	48.8	2	184
HIBEC79	703000	383	HMMER 2.1.1	PFAM: RhoGAP domain	PF00620	114.9	402	884
HOQBF64	703177	384	HMMER 2.1.1	PFAM: RhoGAP domain	PF00620	28.9	302	391
			HMMER 2.1.1	PFAM: RhoGAP domain	PF00620	31.2	308	99
			HMMER	PFAM: Regulator of G	PF00615	38.9	48	167

HTEDL38	761609	385	2.1.1	protein signaling domain	PF00536	56.3	256	441
HE9HI71	779375	386	HMMER 2.1.1	PFAM: SAM domain (Sterile alpha motif)	PF00536	67.7	290	466
HNFS82	779946	387	HMMER 2.1.1	PFAM: SAM domain (Sterile alpha motif)	PF00787	28.7	53	259
HOUHO89	786548	388	HMMER 2.1.1	PFAM: RhoGEF domain	PF00621	56	463	750
HFPBB28	844526	389	HMMER 2.1.1	PFAM: Domain found in bacterial signal proteins	PF00672	43	60	236
HHEWQ61	876063	390	HMMER 2.1.1	PFAM: PX domain	PF00787	36.5	135	353
HUFGH09	877078	391	HMMER 2.1.1	PFAM: PX domain	PF00787	58.6	363	638
HLICA79	880881	392	HMMER 2.1.1	PFAM: Domain found in Dishevelled, Egl-10, and Pleckstrin	PF00610	79.9	103	327
HSLIH01	884251	393	HMMER 2.1.1	PFAM: Domain found in Dishevelled, Egl-10, and Pleckstrin	PF00610	30.9	83	304
HE9OV91	887364	394	HMMER 2.1.1	PFAM: SPRY domain	PF00622	80.6	313	633
HHEDS85	894602	395	HMMER 2.1.1	PFAM: RhoGAP domain	PF00620	26.2	11	121
HNTDJ68	899624	396	HMMER 2.1.1	PFAM: SAM domain (Sterile alpha motif)	PF00536	42.3	1375	1569
HKAHO77	906671	397	HMMER 2.1.1	PFAM: RhoGAP domain	PF00620	24.7	63	248
			blastx.14	GTPASE-ACTIVATING PROTEIN [Homo	gi 2276308 emb CAB 06085.1	69% 95%	64 180	171 248

HTFNP84	909687	398	HMMER 2.1.1 blastx.14	sapiens]	PFAM: RhoGEF domain	PF00621		95% 100% 72% 81% 81% 81%	248 417 313 497 4 481	319 479 366 544 36 513
HDQGZ78	909735	399	HMMER 2.1.1 blastx.14	ect2 [Mus musculus]		gi 293332 gb AAA37536.1		91% 62% 100% 17%	73 1042 27 62	1131 1227 56 265
			HMMER 2.1.1 blastx.14	(AF038388) actin-filament binding protein Frabin [Rattus norvegicus]	PFAM: RhoGEF domain	PF00621		85.2	5	277
HHEMD52	909742	400	HMMER 2.1.1 blastx.14		(AF038388) actin-filament binding protein Frabin [Rattus norvegicus]	gi 3342246 gb AAC27698.1		93%	5	442
			HMMER 2.1.1 blastx.14	PFAM: RhoGEF domain	PFAM: RhoGEF domain	PF00621		64.3	1295	1501
HSIDQ38	909854	401	HMMER 2.1.1 blastx.14	(AF017369) faciogenital dysplasia protein 3 [Mus musculus]		gi 3599942 gb AAC35431.1		70% 62% 100% 80% 77%	998 854 1516 815 1573	1510 982 1545 844 1599
			HMMER 2.1.1 blastx.14	PFAM: RhoGAP domain	PFAM: RhoGAP domain	PF00620		175.6	270	686
				carboxyl terminus of the predicted protein shows 1 comes from this gene; cDNA EST EMBL:D32994 comes from this gene		gi 3874826 emb CAA86318.1		37% 55% 25% 33%	381 270 654 14	659 350 737 67

HSKBF02	909855	402	HMMER 2.1.1 blastx.14	PFAM: RhoGAP domain p115 [Homo sapiens]	PF00620 gi 840786 emb CAA5 5394.1	130.6	9	386
						59%	6	386
						66%	364	390
HIBDE74	909876	621	HMMER 2.1.1 blastx.14	PFAM: RhoGEF domain (AB001770) PEM-2 [Ciona savignyi]	PF00621 gi 4107011 dbj BAA3 6290.1	152.7	44	604
						58%	428	628
						41%	161	421
						33%	29	127
HWMAE53	909877	404	HMMER 2.1.1 blastx.14	PFAM: RhoGEF domain (AF132481) Ese1L protein [Mus musculus]	PF00621 gi 4378891 gb AAD1 9749.1	53	112	267
						44%	112	285
HFXCG28	909961	405	HMMER 2.1.1 blastx.14	PFAM: RasGEF domain (AL080117) hypothetical protein [Homo sapiens]	PF00617 gi 5262547 emb CAB 45716.1	162.7	225	593
						98%	225	593
						50%	149	220
HFTCU45	910053	406	HMMER 2.1.1 blastx.14	PFAM: RhoGEF domain Trio [Homo sapiens]	PF00621 gi 3522970 gb AAC3 4245.1	80.9	82	474
						70%	1	501
						41%	34	387
						35%	421	540
						57%	488	529
HFTBL33	910055	407	HMMER 2.1.1 blastx.14	PFAM: RhoGEF domain (AF091395) Trio isoform [Homo sapiens]	PF00621 gi 3644048 gb AAC4 3042.1	40.3	223	387
						60%	199	483
						61%	31	207
						52%	703	840
						67%	586	687
						33%	598	786
						42%	334	483

HTXJA84	911387	408	HMMER 2.1.1 blastx.14	PFAM: Fes/CIP4 homology domain macrophage actin- associated-tyrosine- phosphorylated protein [Mus musculus]			31% 47% 35% 46%	37 199 1128 1175	189 267 1187 1219
HKAAW89	911389	409	HMMER 2.1.1	PFAM: Fes/CIP4 homology domain		PF00611	42.2	101	373
HSXDD55	911460	410	HMMER 2.1.1 blastx.14	PFAM: RasGEF domain similar to phorbol ester and DAG binding domain; 1		gi 3947712 emb CAA 77027.1	88% 82% 60%	80 592 725	604 726 808
HUFCI64	911558	411	HMMER 2.1.1 blastx.14	PFAM: RhoGAP domain PFAM: RhoGAP domain		PF00611 PF00617	44.7 146.2	88 333	345 695
HWAFT84	911559	412	HMMER 2.1.1 blastx.14	PFAM: RhoGAP domain similar to C.elegans protein (Z37093) [Homo sapiens]		gi 3876235 emb CAA 94755.1	38% 56%	285 857	608 904
HETCL18	914535	413	HMMER 2.1.1 blastx.2	PFAM: RhoGAP domain similar to C.elegans protein (Z37093) [Homo sapiens] PFAM: Domain found in Dishevelled, Egl-10, and Pleckstrin (AF115480) cAMP-		PF00620 gi 1504026 dbj BAA1 3212.1 gi 1504026 dbj BAA1 3212.1 PF00610 gb AAD09132.1	158 87% 50% 34.3 90% 79.9 39%	3 3 8 34 40 16 28	500 773 43 135 702 240 276

HCRNK75	914536	414	HMMER 2.1.1 blastx.2	dependent Rap1 guanine- nucleotide exchange factor [Mus musculus] PFAM: Domain found in Dishevelled, Egl-10, and Pleckstrin (AF115480) cAMP- dependent Rap1 guanine- nucleotide exchange factor [Mus musculus]	PF00610 gb AAD09132.1	79.9 36% 35%	2006 226 1707	1782 525 1790
HTPFA03	922765	415	HMMER 2.1.1 blastx.14	PFAM: RhoGAP domain (AC004794) F02569_2 [Homo sapiens]	PF00620 gi 3184264 gb AAC1 8917.1	54.5 84%	2 50	292 295
HWADR60	926487	416	HMMER 2.1.1 blastx.14	PFAM: RhoGAP domain (AF003389) contains similarity to N-chimaerins [Caenorhabditis elegans]	PF00620 gi 2088864 gb AAC7 1136.1	148.8 33% 30%	153 297 33	605 611 275
HWLFJ01	928017	417	HMMER 2.1.1 blastx.14	PFAM: Phosphotyrosine interaction domain (PTB/PID). (AL117654) hypothetical protein [Homo sapiens]	PF00640 gi 5912247 emb CAB 56030.1	40.6 91% 46% 37%	202 43 691 683	612 675 774 763
HTXNG95	928577	418	HMMER 2.1.1 blastx.14	PFAM: SPRY domain zinc finger protein [Mus musculus]	PF00622 gi 406748 emb CAA5 3092.1	105.7 57% 54% 61%	208 139 52 541	585 492 123 579
HPCIG66	930886	419	HMMER	PFAM: SPRY domain	PF00622	80.4	90	455

			2.1.1	(AC007019) hypothetical protein [Arabidopsis thaliana]	gi 4417294 gb AAD20419.1	46%	57	377
			blastx.14			51%	378	464
						50%	825	866
						38%	550	603
						52%	780	830
HCRPU72	931140	420	HMMER 2.1.1	PFAM: RhoGAP domain	PF00620	94.9	314	715
			blastx.2	similar to human GTPase-activating protein(A49869) [Homo sapiens]	dbj BAA13442.1	97%	77	799
HE9RT95	934556	421	HMMER 2.1.1	PFAM: RhoGAP domain	PF00620	36.8	1	231
			blastx.14	carboxyl terminus of the predicted protein shows 1 comes from this gene; cDNA EST EMBL:D32994 comes from this gene	gi 3874826 emb CAA86318.1	34%	1	237
HFXJM13	935725	422	HMMER 2.1.1	PFAM: PX domain	PF00787	35.8	85	393
			blastx.14	similar to RNA recognition motif. (aka RRM, RBD, or 1 1	gi 3879784 emb CAA93419.1	41%	184	348
						40%	66	155
HDPWU37	940705	423	HMMER 2.1.1	PFAM: RhoGAP domain	PF00620	50.2	3	116
			blastx.14	similar to SH3-binding protein [Homo sapiens]	gi 4826478 emb CAB42896.1	79%	3	491
						77%	503	529
						66%	509	535
HHSDL85	942246	424	HMMER 2.1.1	PFAM: RasGEF domain	PF00617	31	2	55

			blastx.2	(AF053308) putative guanine nucleotide releasing factor [Drosophila affinis]	gb AAC06257.1	50%	2	472
HTJMD31	942848	425	HMMER 2.1.1	PFAM: SPRY domain	PF00622	40.2	58	423
			blastx.14	(AL117386) putative protein [Arabidopsis thaliana]	gi 5881779 emb CAB 55697.1	33%	49	279
HWADD57	943039	426	HMMER 2.1.1	PFAM: GTPase-activator protein for Ras-like GTPase	PF00616	56.1	212	343
			blastx.14	(AB016962) synGAP-b1 [Rattus norvegicus]	gi 4417207 dbj BAA7 4972.1	45% 69% 35%	116 2 739	598 70 855
HLWAH05	944904	427	HMMER 2.1.1	PFAM: RhoGAP domain	PF00620	224.3	470	925
			blastx.2	dJ37E16.2 (SH3-domain binding protein 1) [Homo sapiens]	emb CAB42896.1	96% 98% 41% 31% 26% 30% 37% 28% 26% 30% 20% 26%	413 66 1103 1091 1091 1100 1103 733 1040 721 1046 999	1291 428 1249 1258 1327 1273 1228 924 1258 834 1267 1136
HDPCI84	945527	428	HMMER 2.1.1	PFAM: RhoGAP domain	PF00620	103.4	85	519
			blastx.2	(AK001174) unnamed	dbj BAA91533.1	43%	64	882

HBXDJ07	946830	429	HMMER 2.1.1 blastx.2	protein product [Homo sapiens] PFAM: Synaptophysin / synaptoporin synaptoporin - rat	PF01284 pir JH0300 JH0300	406.7 90% 91%	125 125 610	604 643 921
HAMFD12	952438	430	HMMER 2.1.1 blastx.14	PFAM: Guanine nucleotide exchange factor for Ras-like GTPases; N-terminal motif guanine nucleotide dissociation stimulator [Mus musculus]	PF00618 gi 193573 gb AAA37714.1	40.7 84%	3 3	77 434
HFKHR40	952470	431	HMMER 2.1.1 blastx.14	PFAM: RhoGAP domain carboxyl terminus of the predicted protein shows 1 comes from this gene; cDNA EST EMBL:D32994 comes from this gen	PF00620 gi 3874826 emb CAA86318.1	88.9 46% 49% 81% 47% 37% 23% 37% 50%	1376 1319 1683 1583 232 1253 962 1211 643	1708 1498 1865 1630 300 1324 1078 1282 696
HDTAI08	953265	432	HMMER 2.1.1	PFAM: SAM domain (Sterile alpha motif)	PF00536	29.1	367	534
HMKCX80	956254	433	HMMER 2.1.1 blastx.14	PFAM: PX domain Unknown gene product [Homo sapiens]	PF00787 gi 3417291 gb AAC31664.1	47.3 96% 68%	425 613 533	613 699 607
HCEMF69	961308	434	HMMER 2.1.1	PFAM: PX domain	PF00787	54.8	14	247

HWLHF10	963422	435	HMMER 2.1.1 blastx.14	PFAM: RhoGAP domain	PF00620	121	640	975
				similar to SH3-binding protein [Homo sapiens]	gi 4826478 emb CAB42896.1	49% 43% 39% 68% 30%	661 349 118 592 536	978 591 339 696 604
HOEMG82	963855	436	HMMER 2.1.1	PFAM: IQ calmodulin-binding motif	PF00612	64.9	230	292
HFXDR37	965915	437	HMMER 2.1.1 blastx.14	PFAM: PX domain (AF121862) sorting nexin 13 [Homo sapiens]	PF00787 gi 4689264 gb AAD27835.1 AF121862_1	39.9 35% 36% 33%	1437 957 1002 2263	1189 631 928 2174
HNNAS46	969470	438	HMMER 2.1.1 blastx.14	PFAM: PX domain (AF121858) sorting nexin 8 [Homo sapiens]	PF00787 gi 4689256 gb AAD27831.1 AF121858_1	70.2 99% 99%	232 770 136	573 1435 768
HRAAS26	971219	439	HMMER 2.1.1 blastx.14	PFAM: PX domain (AF139461) hypothetical protein SBB131 [Homo sapiens]	PF00787 gi 4894946 gb AAD32668.1 AF139461_1	52.9 100%	89 59	367 499
HHEEL28	973096	440	HMMER 2.1.1 blastx.14	PFAM: GTPase-activator protein for Ras-like GTPase (AF047711) nGAP [Homo sapiens]	PF00616 gi 4105589 gb AAD04814.1	47.4 51%	148 4	372 375
HCETF22	973324	441	HMMER 2.1.1	PFAM: Diacylglycerol kinase catalytic domain (presumed)	PF00781	202.1	112	468

[60] Table 2 further characterizes certain encoded polypeptides of the invention, by providing the results of comparisons to protein and protein family databases. The first column provides a unique clone identifier, "Clone ID NO:", corresponding to a cDNA clone disclosed in Table 1A. The second column provides the unique contig identifier, "Contig ID:" which allows correlation with the information in Table 1A. The third column provides the sequence identifier, "SEQ ID NO:", for the contig polynucleotide sequences. The fourth column provides the analysis method by which the homology/identity disclosed in the Table was determined. The fifth column provides a description of the PFAM/NR hit identified by each analysis. Column six provides the accession number of the PFAM/NR hit disclosed in the fifth column. Column seven, score/percent identity, provides a quality score or the percent identity, of the hit disclosed in column five. Comparisons were made between polypeptides encoded by polynucleotides of the invention and a non-redundant protein database (herein referred to as "NR"), or a database of protein families (herein referred to as "PFAM"), as described below.

[61] The NR database, which comprises the NBRF PIR database, the NCBI GenPept database, and the SIB SwissProt and TrEMBL databases, was made non-redundant using the computer program nrdb2 (Warren Gish, Washington University in Saint Louis). Each of the polynucleotides shown in Table 1A, column 3 (e.g., SEQ ID NO:X or the 'Query' sequence) was used to search against the NR database. The computer program BLASTX was used to compare a 6-frame translation of the Query sequence to the NR database (for information about the BLASTX algorithm please see Altshul et al., J. Mol. Biol. 215:403-410 (1990); and Gish and States, Nat. Genet. 3:266-272 (1993). A description of the sequence that is most similar to the Query sequence (the highest scoring 'Subject') is shown in column five of Table 2 and the database accession number for that sequence is provided in column six. The highest scoring 'Subject' is reported in Table 2 if (a) the estimated probability that the match occurred by chance alone is less than $1.0e-07$, and (b) the match was not to a known repetitive element. BLASTX returns alignments of short polypeptide segments of the Query and Subject sequences which share a high degree of similarity; these segments are known as High-Scoring Segment Pairs or HSPs. Table 2 reports the degree of similarity between the Query and the Subject for each HSP as a percent identity in Column 7. The percent identity is determined by dividing the number of exact matches between the two aligned sequences in the HSP, dividing by the number of Query amino acids in the HSP and multiplying by 100.

The polynucleotides of SEQ ID NO:X which encode the polypeptide sequence that generates an HSP are delineated by columns 8 and 9 of Table 2.

[62] The PFAM database, PFAM version 2.1, (Sonnhammer et al., Nucl. Acids Res., 26:320-322, 1998)) consists of a series of multiple sequence alignments; one alignment for each protein family. Each multiple sequence alignment is converted into a probability model called a Hidden Markov Model, or HMM, that represents the position-specific variation among the sequences that make up the multiple sequence alignment (see, e.g., Durbin et al., *Biological sequence analysis: probabilistic models of proteins and nucleic acids*, Cambridge University Press, 1998 for the theory of HMMs). The program HMMER version 1.8 (Sean Eddy, Washington University in Saint Louis) was used to compare the predicted protein sequence for each Query sequence (SEQ ID NO:Y in Table 1A) to each of the HMMs derived from PFAM version 2.1. A HMM derived from PFAM version 2.1 was said to be a significant match to a polypeptide of the invention if the score returned by HMMER 1.8 was greater than 0.8 times the HMMER 1.8 score obtained with the most distantly related known member of that protein family. The description of the PFAM family which shares a significant match with a polypeptide of the invention is listed in column 5 of Table 2, and the database accession number of the PFAM hit is provided in column 6. Column 7 provides the score returned by HMMER version 1.8 for the alignment. Columns 8 and 9 delineate the polynucleotides of SEQ ID NO:X which encode the polypeptide sequence which show a significant match to a PFAM protein family.

[63] As mentioned, columns 8 and 9 in Table 2, "NT From" and "NT To", delineate the polynucleotides of "SEQ ID NO:X" that encode a polypeptide having a significant match to the PFAM/NR database as disclosed in the fifth column. In one embodiment, the invention provides a protein comprising, or alternatively consisting of, a polypeptide encoded by the polynucleotides of SEQ ID NO:X delineated in columns 8 and 9 of Table 2. Also provided are polynucleotides encoding such proteins, and the complementary strand thereto.

[64] The nucleotide sequence SEQ ID NO:X and the translated SEQ ID NO:Y are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and described further below. For instance, the nucleotide sequences of SEQ ID NO:X are useful for designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the cDNA contained in Clone ID NO:Z. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling immediate applications in chromosome mapping, linkage analysis, tissue identification and/or typing,

and a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y may be used to generate antibodies which bind specifically to these polypeptides, or fragments thereof, and/or to the polypeptides encoded by the cDNA clones identified in, for example, Table 1A.

[65] Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).

[66] Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X, and a predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing cDNA Clone ID NO:Z (deposited with the ATCC on October 5, 2000, and receiving ATCC designation numbers PTA 2574 and PTA 2575; deposited with the ATCC on January 5, 2001, and having depositor reference numbers TS-1, TS-2, AC-1, and AC-2; and/or as set forth, for example, in Table 1A, 6 and 7). The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. Further, techniques known in the art can be used to verify the nucleotide sequences of SEQ ID NO:X.

[67] The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

RACE Protocol For Recovery of Full-Length Genes

[68] Partial cDNA clones can be made full-length by utilizing the rapid amplification of cDNA ends (RACE) procedure described in Frohman, M.A., et al., Proc. Nat'l. Acad. Sci. USA, 85:8998-9002 (1988). A cDNA clone missing either the 5' or 3' end can be reconstructed to include the absent base pairs extending to the translational start or stop codon, respectively. In some cases, cDNAs are missing the start codon of translation,

therefor. The following briefly describes a modification of this original 5' RACE procedure. Poly A+ or total RNA is reverse transcribed with Superscript II (Gibco/BRL) and an antisense or complementary primer specific to the cDNA sequence. The primer is removed from the reaction with a Microcon Concentrator (Amicon). The first-strand cDNA is then tailed with dATP and terminal deoxynucleotide transferase (Gibco/BRL). Thus, an anchor sequence is produced which is needed for PCR amplification. The second strand is synthesized from the dA-tail in PCR buffer, Taq DNA polymerase (Perkin-Elmer Cetus), an oligo-dT primer containing three adjacent restriction sites (XhoI, SalI and ClaI) at the 5' end and a primer containing just these restriction sites. This double-stranded cDNA is PCR amplified for 40 cycles with the same primers as well as a nested cDNA-specific antisense primer. The PCR products are size-separated on an ethidium bromide-agarose gel and the region of gel containing cDNA products the predicted size of missing protein-coding DNA is removed. cDNA is purified from the agarose with the Magic PCR Prep kit (Promega), restriction digested with XhoI or SalI, and ligated to a plasmid such as pBluescript SKII (Stratagene) at XhoI and EcoRV sites. This DNA is transformed into bacteria and the plasmid clones sequenced to identify the correct protein-coding inserts. Correct 5' ends are confirmed by comparing this sequence with the putatively identified homologue and overlap with the partial cDNA clone. Similar methods known in the art and/or commercial kits are used to amplify and recover 3' ends.

[69] Several quality-controlled kits are commercially available for purchase. Similar reagents and methods to those above are supplied in kit form from Gibco/BRL for both 5' and 3' RACE for recovery of full length genes. A second kit is available from Clontech which is a modification of a related technique, SLIC (single-stranded ligation to single-stranded cDNA), developed by Dumas et al., *Nucleic Acids Res.*, 19:5227-32 (1991). The major differences in procedure are that the RNA is alkaline hydrolyzed after reverse transcription and RNA ligase is used to join a restriction site-containing anchor primer to the first-strand cDNA. This obviates the necessity for the dA-tailing reaction which results in a polyT stretch that is difficult to sequence past.

[70] An alternative to generating 5' or 3' cDNA from RNA is to use cDNA library double-stranded DNA. An asymmetric PCR-amplified antisense cDNA strand is synthesized with an antisense cDNA-specific primer and a plasmid-anchored primer. These primers are removed and a symmetric PCR reaction is performed with a nested cDNA-specific antisense primer and the plasmid-anchored primer.

RNA Ligase Protocol For Generating The 5' or 3' End Sequences To Obtain Full Length Genes

[71] Once a gene of interest is identified, several methods are available for the identification of the 5' or 3' portions of the gene which may not be present in the original cDNA plasmid. These methods include, but are not limited to, filter probing, clone enrichment using specific probes and protocols similar and identical to 5' and 3' RACE. While the full length gene may be present in the library and can be identified by probing, a useful method for generating the 5' or 3' end is to use the existing sequence information from the original cDNA to generate the missing information. A method similar to 5' RACE is available for generating the missing 5' end of a desired full-length gene. (This method was published by Fromont-Racine et al., *Nucleic Acids Res.*, 21(7):1683-1684 (1993)). Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcript and a primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest, is used to PCR amplify the 5' portion of the desired full length gene which may then be sequenced and used to generate the full length gene. This method starts with total RNA isolated from the desired source, poly A RNA may be used but is not a prerequisite for this procedure. The RNA preparation may then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase if used is then inactivated and the RNA is treated with tobacco acid pyrophosphatase in order to remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase. This modified RNA preparation can then be used as a template for first strand cDNA synthesis using a gene specific oligonucleotide. The first strand synthesis reaction can then be used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the gene of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the relevant gene.

[72] The present invention also relates to vectors or plasmids which include such DNA sequences, as well as the use of the DNA sequences. The material deposited with the ATCC (deposited with the ATCC on October 5, 2000, and receiving ATCC designation numbers

PTA 2574 and PTA 2575; deposited with the ATCC on January 5, 2001, and receiving ATCC designation numbers TS-1, TS-2, AC-1, and AC-2; and/or as set forth, for example, in Table 1A, Table 6, or Table 7) is a mixture of cDNA clones derived from a variety of human tissue and cloned in either a plasmid vector or a phage vector, as described, for example, in Table 7. These deposits are referred to as "the deposits" herein. The tissues from which some of the clones were derived are listed in Table 7, and the vector in which the corresponding cDNA is contained is also indicated in Table 7. The deposited material includes cDNA clones corresponding to SEQ ID NO:X described, for example, in Table 1A (Clone ID NO:Z). A clone which is isolatable from the ATCC Deposits by use of a sequence listed as SEQ ID NO:X, may include the entire coding region of a human gene or in other cases such clone may include a substantial portion of the coding region of a human gene. Furthermore, although the sequence listing may in some instances list only a portion of the DNA sequence in a clone included in the ATCC Deposits, it is well within the ability of one skilled in the art to sequence the DNA included in a clone contained in the ATCC Deposits by use of a sequence (or portion thereof) described in, for example Tables 1A or 2 by procedures hereinafter further described, and others apparent to those skilled in the art.

[73] Also provided in Table 7 is the name of the vector which contains the cDNA clone. Each vector is routinely used in the art. The following additional information is provided for convenience.

[74] Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128, 256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., *Nucleic Acids Res.* 16:7583-7600 (1988); Altling-Mees, M. A. and Short, J. M., *Nucleic Acids Res.* 17:9494 (1989)) and pBK (Altling-Mees, M. A. et al., *Strategies* 5:58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Phagemid pBS may be excised from the Lambda Zap and Uni-Zap XR vectors, and phagemid pBK may be excised from the Zap Express vector. Both phagemids may be transformed into *E. coli* strain XL-1 Blue, also available from Stratagene.

[75] Vectors pSport1, pCMVSPORT 1.0, pCMVSPORT 2.0 and pCMVSPORT 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, also available from Life Technologies. See, for instance, Gruber, C. E., et al., *Focus*

15:59- (1993). Vector lafmid BA (Bento Soares, Columbia University, New York, NY) contains an ampicillin resistance gene and can be transformed into *E. coli* strain XL-1 Blue. Vector pCR[®]2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, available from Life Technologies. See, for instance, Clark, J. M., *Nuc. Acids Res.* 16:9677-9686 (1988) and Mead, D. *et al.*, *Bio/Technology* 9: (1991).

[76] The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, and/or the deposited clone (Clone ID NO:Z). The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include preparing probes or primers from the disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.

[77] Also provided in the present invention are allelic variants, orthologs, and/or species homologs. Procedures known in the art can be used to obtain full-length genes, allelic variants, splice variants, full-length coding portions, orthologs, and/or species homologs of genes corresponding to SEQ ID NO:X or the complement thereof, polypeptides encoded by genes corresponding to SEQ ID NO:X or the complement thereof, and/or the cDNA contained in Clone ID NO:Z, using information from the sequences disclosed herein or the clones deposited with the ATCC. For example, allelic variants and/or species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for allelic variants and/or the desired homologue.

[78] The polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

[79] The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below). It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.

[80] The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified using techniques described herein or otherwise known in the art, such as, for example, by the one-step method described in Smith and Johnson, Gene 67:31-40 (1988). Polypeptides of the invention also can be purified from natural, synthetic or recombinant sources using techniques described herein or otherwise known in the art, such as, for example, antibodies of the invention raised against the polypeptides of the present invention in methods which are well known in the art.

[81] The present invention provides a polynucleotide comprising, or alternatively consisting of, the nucleic acid sequence of SEQ ID NO:X, and/or the cDNA sequence contained in Clone ID NO:Z. The present invention also provides a polypeptide comprising, or alternatively, consisting of, the polypeptide sequence of SEQ ID NO:Y, a polypeptide encoded by SEQ ID NO:X or a complement thereof, a polypeptide encoded by the cDNA contained in Clone ID NO:Z, and/or the polypeptide sequence encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B. Polynucleotides encoding a polypeptide comprising, or alternatively consisting of the polypeptide sequence of SEQ ID NO:Y, a polypeptide encoded by SEQ ID NO:X, a polypeptide encoded by the cDNA contained in Clone ID NO:Z, and/or a polypeptide sequence encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B are also encompassed by the invention. The present invention further encompasses a polynucleotide comprising, or alternatively consisting of, the complement of the nucleic acid sequence of SEQ ID NO:X, a nucleic acid sequence encoding a polypeptide encoded by the complement of the nucleic acid sequence of SEQ ID NO:X, and/or the cDNA contained in Clone ID NO:Z.

[82] Moreover, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in Table 1B column 6, or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in Table 1B column 6, or any combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in Table 1B, column 6, and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in

SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in Table 1B, column 6, and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in Table 1B, column 6, and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

[83] Further, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1), or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1), or any combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1) and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1) and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1) and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides

are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

[84] Further, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1B, column 2), or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1B, column 2), or any combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1B, column 2) and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1B, column 2) and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1B, column 2) and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (See Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

[85] Moreover, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in the same row of Table 1B column 6, or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the

complementary strand(s) of the sequences delineated in the same row of Table 1B column 6, or any combination thereof. In preferred embodiments, the polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in the same row of Table 1B column 6, wherein sequentially delineated sequences in the table (i.e. corresponding to those exons located closest to each other) are directly contiguous in a 5' to 3' orientation. In further embodiments, above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in the same row of Table 1B, column 6, and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in the same row of Table 1B, column 6, and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in the same row of Table 1B, column 6, and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

[86] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B, and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1B, column 2) or fragments or variants thereof. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

[87] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1), and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1A or 1B) or fragments or variants thereof. In preferred embodiments, the delineated sequence(s) and polynucleotide sequence of SEQ ID NO:X correspond to the same Clone ID NO:Z. Polypeptides encoded by these polynucleotides, other polynucleotides

that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

[88] In further specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in the same row of column 6 of Table 1B, and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1A or 1B) or fragments or variants thereof. In preferred embodiments, the delineated sequence(s) and polynucleotide sequence of SEQ ID NO:X correspond to the same row of column 6 of Table 1B. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

[89] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of the sequence of SEQ ID NO:X are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[90] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of a fragment or variant of the sequence of SEQ ID NO:X are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[91] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of the sequence of SEQ ID NO:X and the 5' 10 polynucleotides of the sequence of one of the sequences delineated in column 6 of Table 1B are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[92] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of a fragment or variant of the sequence of SEQ ID NO:X and the 5' 10 polynucleotides of the sequence of one of the sequences delineated in column 6 of Table 1B are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides, are also encompassed by the invention.

[93] In further specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of another sequence in column 6 are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[94] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of another sequence in column 6 corresponding to the same Clone ID NO:Z (see Table 1B, column 1) are directly contiguous. Nucleic acids which hybridize to the complement of these 20 lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[95] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one sequence in column 6 corresponding to the same contig sequence identifier SEQ ID NO:X (see Table 1B, column 2) are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[96] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of another sequence in column 6 corresponding to the same row are directly contiguous. In preferred embodiments, the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B is directly contiguous with the 5' 10 polynucleotides of the next sequential exon delineated in Table 1B, column 6. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also

encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[97] Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. Accordingly, for each contig sequence (SEQ ID NO:X) listed in the fourth column of Table 1A, preferably excluded are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 and the final nucleotide minus 15 of SEQ ID NO:X, b is an integer of 15 to the final nucleotide of SEQ ID NO:X, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:X, and where b is greater than or equal to a + 14. More specifically, preferably excluded are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a and b are integers as defined in columns 4 and 5, respectively, of Table 3. In specific embodiments, the polynucleotides of the invention do not consist of at least one, two, three, four, five, ten, or more of the specific polynucleotide sequences referenced by the Genbank Accession No. as disclosed in column 6 of Table 3 (including for example, published sequence in connection with a particular BAC clone). In further embodiments, preferably excluded from the invention are the specific polynucleotide sequence(s) contained in the clones corresponding to at least one, two, three, four, five, ten, or more of the available material having the accession numbers identified in the sixth column of this Table (including for example, the actual sequence contained in an identified BAC clone). In no way is this listing meant to encompass all of the sequences which may be excluded by the general formula, it is just a representative example. All references available through these accessions are hereby incorporated by reference in their entirety.

TABLE 3

Clone ID NO: Z	SEQ ID NO: X	Contig ID:	EST Disclaimer Range of a Range of b		Accession #'s
HDPTE21	11	1165861	1 - 4732	15 - 4746	
H6EDR51	12	1197894	1 - 2300	15 - 2314	
HAPRA41	13	1154054	1 - 1264	15 - 1278	
HBXBI07	14	1171958	1 - 339	15 - 353	
HBXCM38	15	910086	1 - 2160	15 - 2174	AI752485, AI804792, AI439106, AI971133, AI991958, AI752484, AI432296, AI478420, AW082819, AI912373, R89026, AA894797, AI554161, AI752414, H13307, AI249165, R61527, N62403, R89727, N47856, AI689339, AI368569, R61583, AI984780, AA219502, H44175, AI802627, AI752415, T32963, AW295386, AA985168, H06745, R40750, M79099, AA203312, R00511, A91842, A91846, A91844, and A91848.
HCE3E50	16	1227586	1 - 3775	15 - 3789	
HCEQD04	17	1150868	1 - 625	15 - 639	
HDPHI92	18	909900	1 - 2933	15 - 2947	AC068341.
HDPLT89	19	962403	1 - 2437	15 - 2451	
HDPSU48	20	1228284	1 - 2902	15 - 2916	
HDPWE80	21	909916	1 - 932	15 - 946	
HDQFY84	22	1092137	1 - 3253	15 - 3267	
HEONQ19	23	930705	1 - 897	15 - 911	
HFCBB56	24	910073	1 - 553	15 - 567	AA339423, and AC068296.
HFKKZ94	25	1163070	1 - 1318	15 - 1332	
HHBGJ53	26	1187668	1 - 388	15 - 402	
HHFJF24	27	1212624	1 - 2787	15 - 2801	
HHFMM10	28	1178801	1 - 1857	15 - 1871	
HHPBA42	29	901921	1 - 899	15 - 913	
HHSP89	30	1217052	1 - 2277	15 - 2291	
HKABX13	31	1167182	1 - 970	15 - 984	
HLTHG77	32	1162409	1 - 392	15 - 406	
HLWBZ09	33	1179714	1 - 1940	15 - 1954	
HLWEH54	34	1227713	1 - 4510	15 - 4524	
HLYAA41	35	1188029	1 - 797	15 - 811	
HLYDV62	36	1154065	1 - 805	15 - 819	
HMCFB47	37	1151498	1 - 796	15 - 810	
HMSOI20	38	1178817	1 - 2431	15 - 2445	
HOENH55	39	1163460	1 - 612	15 - 626	
HPIAI01	40	1078178	1 - 926	15 - 940	
HPJCT50	41	1201773	1 - 1983	15 - 1997	
HPMFE91	42	1164740	1 - 1867	15 - 1881	
HRAED51	43	1090522	1 - 645	15 - 659	
HSMBA19	44	1197925	1 - 2252	15 - 2266	
HSYCY88	45	914775	1 - 1128	15 - 1142	
HTEDW26	46	909749	1 - 1158	15 - 1172	
HTEKD92	47	1090524	1 - 1447	15 - 1461	
HTLDT05	48	1227127	1 - 2672	15 - 2686	
HTPDS90	49	1197926	1 - 1920	15 - 1934	
HTPHM71	50	1194698	1 - 2017	15 - 2031	
HUUAR12	51	1194702	1 - 1704	15 - 1718	
HWAGP22	52	1150195	1 - 1716	15 - 1730	

HWBCE37	53	906968	1 - 418	15 - 432	
HWLFB60	54	1223499	1 - 2867	15 - 2881	
HDPGS16	55	1075725	1 - 447	15 - 461	
HDQDV69	56	937850	1 - 837	15 - 851	AA887783, AW392670, U46341, AL119457, AL119341, AW372827, U46346, AW384394, AW363220, AL119484, AL119497, AL119355, AL119319, AL119324, AL119443, Z99396, U46350, U46351, AL119363, AL119391, AL119444, AL134902, U46347, U46349, AL119483, AL119396, AL134528, AL119418, AL119335, AL119496, AL119439, AL042433, AL119522, AL042965, AL134524, AL119399, AL134920, AL037205, AL119401, U46345, AL134536, AI142132, AL119464, AL042450, AL042614, AL043029, AL134525, AL134538, AI142131, AL042551, AL042984, AL042975, AL042544, AL043019, AL042970, AI142134, AL042542, AL043003, AL119488, AF169035, AF085233, AB026436, AR054110, A81671, AR066494, AR060234, and AR069079.
HE6BK63	57	1153879	1 - 755	15 - 769	
HFKDR14	58	974255	1 - 1721	15 - 1735	AI761729, AW162515, AW104395, AW298361, AI073443, N40162, AI832126, AI827518, AW297353, R52045, AI342317, R71958, AF128625, AF021936, and AB032950.
HFPER82	59	1152249	1 - 619	15 - 633	
HAAAO58	60	1091088	1 - 1309	15 - 1323	
HADFK69	61	1091937	1 - 1603	15 - 1617	
HDPMO62	62	1152329	1 - 1123	15 - 1137	
HDPMO85	63	1228282	1 - 2479	15 - 2493	
HDPUY72	64	1228285	1 - 3040	15 - 3054	
HDTJF87	65	1154640	1 - 826	15 - 840	
HE8TB94	66	1178794	1 - 1913	15 - 1927	
HE8UB55	67	1228113	1 - 3332	15 - 3346	
HEBGA65	68	1178633	1 - 1803	15 - 1817	
HEGBB59	69	1197907	1 - 2465	15 - 2479	
HELHC48	70	956003	1 - 803	15 - 817	
HEOQH90	71	1212646	1 - 2609	15 - 2623	
HFKHA18	72	1152242	1 - 1055	15 - 1069	
HFKMA10	73	964258	1 - 960	15 - 974	
HHBFM91	74	1092116	1 - 901	15 - 915	
HIBBF63	75	912715	1 - 950	15 - 964	AC012171, AC012171, AC012171, AC009065, AC009065, AC009065, AC005346, AC005346, and AC005346.
HMCEI38	76	1134410	1 - 613	15 - 627	
HMWJD68	77	1154790	1 - 1350	15 - 1364	
HOEOL58	78	1078090	1 - 778	15 - 792	
HRACA51	79	1162856	1 - 1075	15 - 1089	
HSHAV32	80	1180388	1 - 2589	15 - 2603	
HTPDE66	81	971281	1 - 479	15 - 493	
HTPDV73	82	997659	1 - 411	15 - 425	
HTPHE33	83	1163871	1 - 1714	15 - 1728	
HUFDN58	84	1224609	1 - 2404	15 - 2418	
HUVFX92	85	1225329	1 - 428	15 - 442	

HWAEG71	86	1182321	1 - 1471	15 - 1485	
HWAHD49	87	1228064	1 - 1365	15 - 1379	
HWLGG31	88	1178825	1 - 2007	15 - 2021	
HWLKF25	89	1089052	1 - 1097	15 - 1111	
H2CBH45	90	963811	1 - 470	15 - 484	AA307462, AA036880, AL133047, D89677, AC068243, and AC068243.
HAGDN53	91	1092161	1 - 1702	15 - 1716	
HAMFM39	92	971347	1 - 4593	15 - 4607	AI951619, AI814592, AI745391, AI922346, AA426190, AW105735, AW297557, AI829867, AI971865, AA227834, AW028756, AA151872, AA757072, AI202419, AW176248, AW295401, AI659079, AA149658, AA425159, AI765117, AI870033, AW194075, AA233413, AW102818, R61588, AA365664, AA365663, AA601170, R61532, AA357346, AA551861, AI660231, AI467782, Z99396, AW392670, AL119324, AL119319, U46350, U46351, AL119457, AL119484, AL119391, U46347, AW372827, AL119522, AL119439, AL119335, AW384394, AL119483, AW363220, AL119363, AL119497, U46349, AL119355, AL119444, AL119443, U46341, AL134518, AL134525, AL119341, AL037205, AL119401, U46346, AL119396, AL134538, AL134531, AL134528, AL119418, AL119496, AL119399, U46345, AL134524, AL042544, AL042614, AL042984, AL042542, AL043019, AL042450, AL134542, AL043003, AL042965, AL042975, AL043029, AL042551, AL119464, I05430, I05393, A10617, AR028792, AR028791, AR028793, I25027, AR054109, I44515, I26928, I26930, I26927, I25041, I44516, A01324, AR035224, AR009151, I85513, AR009152, A01323, AR027099, AR034783, A94046, A94054, I63120, AR067733, AR064322, AR064323, AR064320, AR064321, A32110, A94048, A94061, A49045, AR038321, A83642, AR019094, A83643, A70359, A92666, AR038307, A92668, A92667, I49890, A92665, A92081, A92080, A92077, A92078, A92079, AR018924, AR018923, A48774, A48775, AR000006, AR015960, AR015961, AR000007, A91752, A91751, AR051652, A85308, AR068508, AR068510, AR068509, I91969, A91754, I58322, I58323, AR003585, A63067, A51047, A63064, A63072, AR031375, AR068507, A60213, AR068506, AR062871, A44171, AR068550, A23373, AR068551, A49700, A60207, A60208, A29109, A32111, I58669, A58521, AR031374, I07209, I07249, A63954, AR051651, AR019097, AR019098, AR019096, AR029417, I77227, AR020199, AR020200, AR001287, AR020198, AR020197, I89986, AR051957, AR029418, AR067734, AR067731, AR067732, Y14971,

					A93444, A46342, A46343, AB026436, I09121, AR032878, AR060234, AR066494, A81671, AR054110, and AR069079.
HBGQT03	93	908173	1 - 1196	15 - 1210	AW193981, AA576536, AW439879, AA218860, AA587394, AI735027, AW206358, AI075695, AI749755, AI073515, AI283940, AI828816, AW328242, AA452508, AI741698, F25077, AA454093, AI280249, AI826261, AI567379, AA350150, AI251129, F26225, AI354257, AA171893, AW129660, AI357160, F26293, F36700, H24638, AI270014, AI952189, AA834233, AI689497, AI688448, F17480, Z38509, T11668, N93072, AW362737, T11669, AW273866, N93071, AW328241, AF130979, AC024045, AC024045, and AC024045.
HBGSJ13	94	1150790	1 - 808	15 - 822	
HBIBQ89	95	909782	1 - 851	15 - 865	AA399613, F11248, Z42117, AA082253, F05395, T35421, and AB007925.
HCECM90	96	945088	1 - 1379	15 - 1393	AA463356, AA453500, AA322899, AA340682, H24259, AA603868, AA330182, R19782, and AB023227.
HCEPH71	97	522739	1 - 432	15 - 446	AA326209, AA383931, AL365319, and AL390715.
HCFMT57	98	1175204	1 - 2197	15 - 2211	
HCOMM05	99	1173146	1 - 1625	15 - 1639	
HCOOZ11	100	965306	1 - 689	15 - 703	AI350354, AI904299, AI902503, D61534, T78554, AW183962, AI218626, AW304978, W74167, AI081779, AL022238, AL137499, AL022238, AL022238, and AL022238.
HCWFF88	101	506577	1 - 304	15 - 318	AL157951, AL157951, AL157951, and AC025670.
HDMAV01	102	1194696	1 - 1796	15 - 1810	
HDPDA47	103	929193	1 - 1036	15 - 1050	AW402583, AL049683, and AL023653.
HDPFF24	104	909232	1 - 447	15 - 461	AI929099, AI566117, AI928828, N88094, AA365879, AA281290, H67457, N87549, AW450464, AA295368, AA527887, AI033615, AA354369, AA086081, and AA903373.
HDPPO35	105	966248	1 - 1890	15 - 1904	AI640500, AW439548, AI823872, AW297416, AA831672, AI815031, AA994323, AA741162, AA471280, AI223999, AW339548, AW235171, AI635436, AA035703, AA747998, AI371399, N67227, AA361754, AA063573, AI536057, AI357169, R33401, C01451, R33402, AA825399, AF165138, and AF130247.
HDPSR74	106	911396	1 - 709	15 - 723	
HDTKQ14	107	886936	1 - 541	15 - 555	AL023653, AL049683, AL359542, AL359542, and AL359542.
HE6GF02	108	1150897	1 - 790	15 - 804	
HE8PK12	109	909884	1 - 707	15 - 721	AA296029, AL117472, U58883, AF136380, AF136381, AF078667, and AF078666.
HE9SE62	110	911476	1 - 915	15 - 929	AW021430, AI765247, AI822051, AI822104, AA010459, N70537, AL133567, and AB018312.
HEOPL36	111	1195682	1 - 2095	15 - 2109	
HFB DJ13	112	911264	1 - 476	15 - 490	M86084, and AF030131.

HFTDF15	113	657020	1 - 367	15 - 381	AL365277, AL365277, AL365277, AC024511, AC024511, and AC024511.
HHEQV39	114	932851	1 - 873	15 - 887	AA355773, and AA355926.
HHFCK09	115	965304	1 - 2789	15 - 2803	AI218626, AI076006, AW162820, AI797880, AI922744, AI872391, AI559566, AL045117, AW161046, AW162613, AI565503, AW183962, AI857802, AA460810, AI884907, AI371131, AW248493, AI081779, AA460372, AA679085, N27884, AA581796, AA074070, AA971563, AI292006, AI922373, W76538, N93245, AI609183, AW172513, AI904299, AI682939, AA075764, AI885613, AA747871, AA449042, AA928020, AW401847, AA449757, AW268637, AW073851, AW304978, AI683858, AA568598, W74167, AI367698, AW191998, N62781, AW016535, AI902503, AA347639, AA297591, AA379280, AA568887, AA649970, AW264577, AI221886, H20460, AW387087, AW000860, AI275195, AA341002, T32918, AW162711, W25103, AI699657, R42681, AW243790, AA768740, T78554, AI279653, AI560482, AI696251, AI951374, Z45830, AA147203, AI499410, R43259, AI350354, AA732831, AW079129, AA375228, F08622, AI475009, R56337, AA379846, R17163, AW380349, AA783050, AW247402, N47545, R35508, R51077, AI474934, N79729, D61534, Z41466, AI678630, AA339343, AW367003, AA160401, Z41592, AW079321, N47546, AI252528, R58857, T16943, H55297, AL022238, AL137499, and AJ236700.
HISDS62	116	935932	1 - 506	15 - 520	W27339, AA126105, AA306119, W27700, AB007884, and AJ250425.
HLQDT35	117	839777	1 - 516	15 - 530	AA706241, AA707183, AA152440, N99172, AA131985, AA358765, AA253107, R10421, N56752, AA290907, R08557, AA485099, AI091625, AA134742, AL137699, AC010998, AC010998, AC010998, AC013357, AC013357, and AC013357.
HLWFN63	118	908437	1 - 3089	15 - 3103	AA707313, AI880426, AI684827, AI744551, AI307796, AA101249, AI284152, AA007399, N98643, AI375268, N66095, R71685, R02817, AA085724, AI221876, AI061056, AW207571, AA111956, AI460369, AI333887, AA594062, R18624, R62793, W22434, AW007868, AA776586, T70023, R71720, H70803, AA323135, AA101290, AA029721, AA320669, AI193496, R07828, AA007478, AI915644, AI932703, T69946, R62792, AA029660, AI859215, AA205667, AI625446, AI273982, AB018333, AC006599, AL033378, AL033378, AC006599, and AC006599.
HMEFT66	119	856149	1 - 337	15 - 351	
HMSCD15	120	918133	1 - 1223	15 - 1237	AA828277, AI707568, AI333720, W33154, AI880870, AA848014, AA864599, N50622, AW087770, AW270419, AA761244, AA262754, AA779760, AI880826, AW407353, W37119, AA206843, Z42584,

					AA206842, AB011126, AL158207, AL158207, and AC027008.
HMSHO64	121	746582	1 - 398	15 - 412	
HMTAW83	122	911385	1 - 487	15 - 501	AI908321, AA831896, AR058970, AR058968, A68194, and AR058969.
HMVAM09	123	963814	1 - 1009	15 - 1023	AI685410, AI969804, AA621392, AA358533, AW135812, AI376856, and AI276887.
HNSAA28	124	946988	1 - 1544	15 - 1558	AA713959, AI564093, AA768779, AA825697, AA808021, AA808149, AI401490, AW181992, AW444640, AI018159, AF146277, and AF077003.
HOGEQ43	125	1226207	1 - 4196	15 - 4210	
HOUDH19	126	1150918	1 - 515	15 - 529	
HOUFT36	127	911293	1 - 832	15 - 846	AI806483, AI147946, AA256164, AW236751, AA057615, AW362445, AA542823, AF162130, AC005084, and AF161181.
HPMFL08	128	959569	1 - 452	15 - 466	AA555286, AA640814, AI281916, AW073979, AI378363, R70468, AW242350, AW013856, AA644290, AW449140, Z93016, AC012384, AL035541, AC005228, AC003662, AC009300, and Z93016.
HRSMD49	129	723025	1 - 443	15 - 457	AA136820.
HSDII69	130	917180	1 - 1612	15 - 1626	AA203346, AA203330, AA489694, AI912487, AW024848, AA133454, AA640288, AA658936, Z24863, AA665267, AA878769, AI024792, AI383978, AW022618, T31809, AA318980, T86474, AA669824, AA115749, AW296909, AA552781, AI459513, AI332862, AI332863, and T86475.
HSDSB06	131	949151	1 - 2264	15 - 2278	AW009631, AI765056, AA877550, AA102362, AA625117, AA447454, AA446651, AA724535, AI220147, AA430607, AA019158, AI198643, AW389353, AA516463, AW197881, AA045561, AA186967, H86071, H67029, AW378928, H12433, AA768085, R66487, AA478635, N55248, AA359925, R33870, AA385529, AA054621, AA961423, AW002948, AI802284, AA377365, D31590, AW275740, AI766068, C01179, AL133047, D89677, and AF003234.
HSFAM09	132	1150965	1 - 531	15 - 545	
HSSAX53	133	507509	1 - 348	15 - 362	
HSVAW49	134	1150960	1 - 970	15 - 984	
HTEAG49	135	954614	1 - 1289	15 - 1303	AW452652, AI039005, AA780077, AW316890, AI337290, AA463229, AA463230, AI423317, AI468158, AA382497, N66986, AF041822, AL390796, AL390796, AL357045, and AL357045.
HTLBH67	136	751985	1 - 432	15 - 446	W19592, AC005368, AC008439, AC022420, AC022420, AC022420, AC005368, AC005368, AC008781, and AC008781.
HTLJC71	137	922923	1 - 1738	15 - 1752	AL039539, AL045443, AI336919, AA406128, AA405229, AL042307, AA431504, AA311249, AW086440, AA813520, AI240644, AA897733, AW268487, AA782009, AW172455, AI301209, AI014598, AA969918, AL041043, AA431178,

HOUDS09	176	1164010	1 - 1631	15 - 1645	
HTEGM38	177	675087	1 - 350	15 - 364	
HTEKY82	178	1152495	1 - 486	15 - 500	
HTLCY54	179	1193550	1 - 1049	15 - 1063	
HFOXK14	180	603245	1 - 616	15 - 630	AL096870, and AL096870.
HHFFO69	181	837703	1 - 901	15 - 915	
HHFLU06	182	857884	1 - 316	15 - 330	AL096870, and AL096870.
HAGBA56	183	732597	1 - 653	15 - 667	AA812064, AA430303, AA430200, AI803142, AI425013, AA954361, AB020641, U62391, AF033655, AC006036, AC000057, and AC002458.
HAGGF84	184	911312	1 - 421	15 - 435	AL135568, AJ252239, AF071569, U73504, D14906, J05072, X63615, AC004056, and AC004168.
HAHGD33	185	921782	1 - 1051	15 - 1065	AW378448, AW378426, AA064738, Z43369, AA984486, D31100, W79308, T35774, T08259, W52734, W73106, AI904952, R10018, AA348984, T80752, AA639598, R57404, T81225, AW408302, T81300, R13945, T47464, W79389, Z43504, AA404490, AA196613, W01185, H14918, H45144, and AF113249.
HAHIY08	186	962113	1 - 265	15 - 279	AA100160, AA307684, AA244505, R57782, AA864846, AR044133, and AR044123.
HBIOZ10	187	973131	1 - 490	15 - 504	AC010761, and AC010761.
HBKDI30	188	729048	1 - 625	15 - 639	AA197072, R02824, J05194, J03886, and AL160175.
HBXBW40	189	706115	1 - 462	15 - 476	AL023754, AL049688, and D86557.
HCEHE35	190	909937	1 - 378	15 - 392	AB019692.
HCEPW85	191	911374	1 - 302	15 - 316	N83965, AA326737, and H14153.
HCFAT25	192	932068	1 - 579	15 - 593	AI287912, AL134532, AF096300, AB014587, AC005035, AL137755, and U88984.
HCFCF47	193	1139731	1 - 980	15 - 994	
HDAAV61	194	810305	1 - 329	15 - 343	AI762433, AI191825, AA159268, AA083866, AW105372, AA157878, AI140935, AI922109, AA158846, AA488548, AI187149, AA442140, AA837990, AI494201, AL048644, AI366974, AI537837, AA425228, AW410089, AL038605, AI821259, AW084097, AW083168, AI624304, AI918554, AA508692, AI918634, AI307494, AI349622, AI738867, AI310571, AI802372, AI918408, AW021662, AI348897, AI366959, AW058233, AI345397, AL038564, AW089275, AI340511, AA857847, AI446405, AI799305, AW022494, AW020288, AI281867, AI312210, AI307569, AI270295, N71180, AI702301, N75771, AL036652, AW021373, AL036856, AI312428, AI866820, AW059713, AI889147, N27632, AI336513, AW022102, AA019646, AI348895, AI313320, AI336495, AI310920, AI307503, AW079736, AW082532, AW089572, AI345143, AI309391, AI955906, AI309431, AI336662, AI868204, AI310575, AI349276, AI307507, N22406, AA420722, AI336565, AI683559, AL040694, AI311440, AI334893, AI349186, AI340533, AW088560, AI690472, AI521005, AI537515, AI493601,

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HDPKD75	195	810824	1 - 524	15 - 538	AA923698, AL040000, AF191838, AR016417, AF191839, and AF145705.
HDPNC96	196	934520	1 - 720	15 - 734	AA256100, and AB023182.
HDPSR15	197	969666	1 - 1218	15 - 1232	AW195239, AW149418, AW005579, AI378013, AA147800, AI436586, AI392913, AW337924, AI377235, AI264931, AI203549, AW104319, AI094031, AA461376, H59980, AW166255, AA508841, AI360737, AA463275, AA417605, AI682196, H59937, AI208175, N30324, AA460078, AW001677, AA514325, N50317, AA741518, AI091790, T11446, AA360254, AI208678, AA214523, D20738, R61563, T12550, T11445, AA428834, AI276889, AB026289, and AR044150.
HDQDX20	198	919027	1 - 1280	15 - 1294	AI905612, N75655, N94726, AA297704, H53438, AW339945, AW405560, AA719945, AI682436, AA971968, AW085268, H67340,

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HDQHB19	199	1226089	1 - 2263	15 - 2277	
HDTBY88	200	934472	1 - 495	15 - 509	AA868305, AI700890, AA789239, AI803004, AI694352, AA043382, F08474, R21498, AF112183, AF112184, and AC005354.
HE2KZ07	201	909948	1 - 1167	15 - 1181	AI141657, AW410635, AI377644, AI373441, AI435842, AI813994, AI222162, AI816276, AA134062, AA115521, AA027340, AI198968, AI936995, AA432023, AI417110, AA019881, AA431770, T33003, AI804202, AW296590, AA894568, AA888588, AI816392, AW157195, AA774185, AI312197, AA770240, AI005469, T15996, AI589559, T83662, AI802351, AA164900, AI637808, AW294821, AI612103, AI452706, R96447, AI214546, AA083117, AI219844, AI312448, AA978205, H98210, AI423512, AA115526, N74543, AI823785, H19250, T16797, AI803155, AW051574, Z41102, AI300274, AA970855, T30646, T78862, T81921, R42142, R38428, R05531, T99321, H16697, R08035, AA114950, H52123, AA114923, R41504, R08085, F18392, D79266, R42920, AI028740, AA114993, F34433, F25527, AA130289, C02151, AL118820, AI696123, H10371, AA954386, T34819, AA135800, AI219437, T81018, AA135799, AI372829, AI056831, H68913, AW051694, AI986390, W28788, H10372, U95740, D86556, AB004267, AB023027, and AF181984.
HE8UY74	202	960914	1 - 553	15 - 567	N23547, H06088, Z24919, R94366, AA010516, AA004981, AA304780, AL356968, and AL356968.
HE9NO66	203	974353	1 - 976	15 - 990	AI732997, AA865818, AA977633, Z69734, AB035267, AB020741, and Z68339.
HEMBT61	204	939957	1 - 449	15 - 463	N86549, AW369713, and AB002301.
HETLF29	205	909762	1 - 404	15 - 418	AA960957, AI001155, and AC004664.
HFIUE75	206	909758	1 - 1104	15 - 1118	AA745592, AA780791, AI680317, AA205127, R06019, AW074511, T76970, AW408392, T86065, T77135, AI709216, R05922, T85884, AA730855, and R77022.
HFKIT06	207	934019	1 - 286	15 - 300	AC026976, AC068353, AC068353, AF284563, AF284563, and AC026976.
HHEGG20	208	894409	1 - 808	15 - 822	AF084205.
HHEHC53	209	921783	1 - 896	15 - 910	AW408302, AW410815, AW161181, AA160313, AA226860, AA044358, AI632654, AA232389, Z43369, AA249020, T35774, AA852244, AA064738, AA295773, D31100, R13945, AA205277, T47464, T08259, AI904952, AF113249, AC009427, AC009427, and AC009427.
HHHERQ79	210	944057	1 - 497	15 - 511	AW340333, AI806295, AW268810, AA827664, AA829237, AA909185,

					AA919008, AA604425, AW407893, AA011359, AL134902, D63485, AB016590, AB016589, and AR043113.
HISAF59	211	959140	1 - 899	15 - 913	AW401787, AI394630, AI418298, AW375742, T30407, Z44281, F07299, R25015, T32685, AA974700, F07734, AA297059, AW239548, AA897415, R45025, AI807678, AI343378, AW206793, AW138409, AW163027, AI815476, AA503315, AA047793, AW137324, AW140018, AI936871, AI015047, AI017077, AI168175, AI302185, AI025217, F03423, R46686, AI073417, Z40806, AA026054, AW002416, AI652375, F03562, T03397, AI983297, H42881, T82311, AI025310, AI831833, R08769, AI911100, AA471062, AW157059, AA382959, H22172, AI356604, AI537006, AI825970, AW338394, AW192088, AI559159, AA593826, AW078709, and Z61277.
HKAKM10	212	918685	1 - 596	15 - 610	AW166113, R88730, AF071071, AF170303, AF170304, AF077658, and AF071070.
HLTHP86	213	919354	1 - 2470	15 - 2484	AA702160, AI457618, AI951809, AI808761, AI911971, AI808636, AI633963, AI092909, AA922021, N53171, AA809486, AI092910, AI253245, AA236950, AI432182, AI093897, AI363415, N50448, AI248799, AA663589, AA235935, AI239417, AA121162, AW270053, AI889821, AW296666, AI263508, N50504, H16878, H09671, AW028355, AW300355, R56761, H84971, AI373750, H16267, Z44040, Z44727, AI025923, N58608, T95750, T34716, AA363673, R43831, AA687486, R91239, AI829631, AA687431, AA852910, H16769, T95749, AI268135, AI686257, R56913, Z40554, AA834548, AA872305, C02338, and AF161420.
HMSJL96	214	934483	1 - 662	15 - 676	R01798.
HMTAJ73	215	813296	1 - 651	15 - 665	AI831613, AI924408, AI870169, AW068406, AI368905, AW168626, AI284115, AA678670, AA568895, H19069, AA627558, AA857431, AJ010119, AF074714, AF074715, AC015698, and AC015698.
HNTCP13	216	909770	1 - 1793	15 - 1807	AI479379, AW273740, AA463847, AI740675, AI014722, AI922082, AA463334, AW009462, AI073540, N95224, AI190238, AA007373, AI798079, AA476563, AA670286, H02882, N92851, AA652716, AW016339, H45475, W25554, AA774170, H45576, AI370125, AI811794, AW119159, H03781, H20952, AA853882, AA853883, AI471060, AW382128, AW371996, W21053, H20991, AA368628, AW138258, AA476448, AA876335, AA788825, AF037447, and AC004486.
HNTMD79	217	934522	1 - 573	15 - 587	AA305176, AL160291, AL160291, AL365228, and AL365228.

HNTMH70	218	757184	1 - 674	15 - 688	H19102, AI699883, AI383263, AC005726, and AC004807.
HNTNB14	219	909942	1 - 644	15 - 658	AA082976, R60839, AA349498, F12661, T74243, L22557, AC068701, and AC068701.
HODFF88	220	974911	1 - 1843	15 - 1857	D80164, D59502, D80193, D80195, D59275, C15076, D80227, D58283, D80022, D80166, D81030, D59859, D51799, D59619, D80210, D80391, D80240, D59787, D51423, D80253, D80043, D80269, D50979, D80212, D80038, D80196, D80024, D80219, D80188, C14331, D59467, D57483, D59927, D80378, D80366, C14389, D59889, D50995, D80045, D59610, AA305409, C14429, D80241, D51060, T03269, C14014, AW178893, C75259, AA305578, D81026, D59695, D51022, AW179328, D81111, AW178775, D80134, AW378532, AW177440, D51250, AW352158, D80268, F13647, AA514188, AW369651, D80251, D80522, D51079, D80248, D80949, D58253, AW178762, D80168, D52291, C14227, AA514186, AI905856, AW177501, AW177511, D80133, Z21582, AW360811, C05695, C14298, AW352117, D80064, AW176467, AW375405, AW378540, C14407, AW377671, D51097, AW366296, D80302, AW360844, AW360817, AW375406, AW378534, AW179332, AW377672, AW179023, AW178905, D80132, AW360834, AA285331, D80439, AW352171, AW377676, AW178906, AW352170, AW177731, D80247, AW178907, AW179019, AW179024, D51103, AW177505, AW360841, AW179020, AW178909, AW177456, AW179329, AW178980, AW177733, AW378528, AW178908, AW178754, AW179018, AW179220, AI557751, AW179004, AW178914, AW378525, AW352174, T11417, D80157, AW177728, D59627, D51759, AW367967, AW178774, AW178911, AW378543, AW352163, D59503, D80258, D80014, C06015, AI557774, AW178983, AW352120, T03116, AW178781, T48593, D58246, C14077, D59653, AW177723, D58101, D45260, AI525923, AW178986, AW367950, C03092, AA809122, H67854, D59551, H67866, C14975, T02974, AW378533, AW378539, D51213, AW177734, AI535686, D59317, D51221, AI525917, C14973, AA514184, C14344, D45273, AI525925, AI525920, D59474, AI525227, D31458, C14046, AI525242, AI525235, T03048, AI525912, AW378542, AI525215, AI525237, C16955, C05763, Z33452, AI535850, AI535961, A84916, AJ132110, A62300, A62298, AR018138, X67155, Y17188, D26022, A25909, A67220, D89785, A78862, D34614, D88547, AF058696, X82626, AR008278, AB028859, AR025207, I82448, Y12724, A82595, AB012117,

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HOHCE47	221	1216683	1 - 2147	15 - 2161	
HPCRV84	222	945856	1 - 475	15 - 489	AA307070, D79997, L76158, and X95351.
HRACK83	223	888037	1 - 566	15 - 580	AC005832.
HRADM45	224	717358	1 - 468	15 - 482	AA418916, AA426580, AJ271722, AP000260, AP000036, AF055919, AP000099, and AP000098.
HRAED74	225	942527	1 - 691	15 - 705	AC005940, L42810, S83194, AF117384, and AB023658.
HRODZ70	226	942673	1 - 572	15 - 586	AA292911, AA167655, AA167766, H97685, AA635138, Z41812, and AB007941.
HSKAC24	227	823869	1 - 498	15 - 512	AF170301, AF170302, AF077659, and AF144573.
HSSMT34	228	911294	1 - 540	15 - 554	AA378627, F07835, and AL117482.
HT3BG12	229	921593	1 - 368	15 - 382	AB028951, and AL122055.
HTEGO05	230	932583	1 - 1086	15 - 1100	AA059465, AA059211, AA731209, AA236961, T86500, T87461, AL024498, and M35862.
HTEKT33	231	953308	1 - 1648	15 - 1662	AW292935, AW027321, AW027332, AI538521, AL040176, H29877, H85389, H29974, H84772, Z41499, AL045794, T24112, T24119, D80253, D80043, AI744745, AL039924, D80219, AW013814, D59275, T10477, D51250, D80240, AA016312, D80227, H00069, D80210, D51423, D80134, AL043441, T02921, D59619, D80193, AL039156, D80391, AL039150, AL043445, AL038821, D59787, AL039509, AL039564, AL039538, AL044530, AL039108, AL039678, D80196, AL039074, AL038837, AL039625, AL039648, AL039629, AL039566, D80045, AL039659, T23947, AL037726, AL038531, D80168, AL039109, AL040992, AL039128, AL044407, AL036973, AL043423, AL045337, AL037051, AL045353, AL036725, AL039386, AL039423, AL045341, AL042909, AL039410, C14227, D80366, AL043422, AL038025, D59927, T11051, D81026, AL039085, AL036196, C14014, D59889, AI535783, AW451070, D80038, C75259, D50995, C15076, AL037639, R47228, D80022, AI535983, AL037526, AL037615, D80195, D80949, D58283,

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HTEMU66	232	944419	1 - 1078	15 - 1092	<p>AL039924, AL045794, AW013814, AL036630, T02921, AL044412, T24119, AL044364, T24112, AW450335, AL039476, D51250, D80253, D80043, AL040992, AL039109, AL038531, AL037726, AL039629, AL039625, AL039648, AL038837, AL039074, AL039678, AL039108, AL039538, AL039564, AL039156, AL039659, AL039566, AL039509, AL039521, H00069, AL039128, AL044407, AL036973, AL045337, AL037051, AL045353, AL039386, AL039423, AL045341, AL042909, AL039410, D59787, AL039150, AL044530, AL038821, AL038025, D80219, AL036725, AL043422, D59275, AL043445, AL039459, AI535983, D80227, AL043586, AL043423, D80240, AL043441, D80210, D51423, T23947, AL036650, D80134, AL036196, D59619, D80391, AL037639, D80193, AW451070, AL037615, D80196, AL036767, C14227, AL039085, AI535783, D80949, AL036117, D80366, D59927, AL037526, AL042334, AW452756, D80168, R47228, AL036238, AL036679, AL037601, T11051, D81026, AL039504, C14014, D50995, C75259, AL039842, AL036964, D80045, AL036733, AL036158, AL037027, AL036924, AL037054, D59889, AL036765,</p>

AL037077

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HTEMV09	233	909843	1 - 1347	15 - 1361	AI818734, AA454060, AA453640, AW268879, AI377304, AI818733, AI818743, AI681535, AI741915, AA948041, AI198872, AW341578, AI267885, AA767746, AI677678, AI829855, AI677729, AW129267, AA947425, AA297313, AL041049, N67346, and AA889773.
HTEMV66	234	1151075	1 - 847	15 - 861	
HTGAU79	235	1175071	1 - 2139	15 - 2153	
HTLEJ11	236	973302	1 - 956	15 - 970	M62294.
HTLIY52	237	1218691	1 - 1362	15 - 1376	
HTOAK34	238	966800	1 - 1271	15 - 1285	AW408167, AA491322, AA505126, AI340133, AA831203, N27153, AA053564, AA809481, AF181985, and AF179867.
HTPGG25	239	911282	1 - 829	15 - 843	AA018361, AI768326, AI333117, AA324901, F07835, AA378627, AL117482, Z61430, AC020705, and AC020705.
HUJAD24	240	1161319	1 - 1722	15 - 1736	
HUTSF11	241	966029	1 - 416	15 - 430	AI384010, AI288640, Z20435, and A74523.
HUVGZ88	242	1227628	1 - 2921	15 - 2935	
HWADY66	243	1096252	1 - 352	15 - 366	
HWAFG04	244	952878	1 - 1646	15 - 1660	AI302185, AI652375, AI936871, AW206793,

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HWAFS18	245	948434	1 - 946	15 - 960	W25237, and AF156884.
HWAGS73	246	1150212	1 - 612	15 - 626	
HWLEA48	247	927676	1 - 415	15 - 429	AA130828, AF169034, Z98752, and AF169033.
HWLHS82	248	934505	1 - 415	15 - 429	AW401390, and AC005581.
HWMIB81	249	955336	1 - 1479	15 - 1493	AW380440, AW299858, AW391525, H78769, H78659, H53674, AA628987, AA447173, AW204470, AA343468, AA480342, AF155118, AC021719, and AC016143.
HCWDV17	250	1105673	1 - 684	15 - 698	
HELDI95	251	1103374	1 - 983	15 - 997	
HAGFO25	252	1150845	1 - 806	15 - 820	
HAWAB54	253	1149319	1 - 1428	15 - 1442	
HLIBV06	254	934887	1 - 2224	15 - 2238	
HMALL66	255	1105097	1 - 495	15 - 509	
HOACE12	256	858976	1 - 439	15 - 453	
HOGCG69	257	924848	1 - 1209	15 - 1223	
HAGAE09	258	1150864	1 - 838	15 - 852	
HAGAE34	259	1121869	1 - 757	15 - 771	
HARMH78	260	1137572	1 - 547	15 - 561	
HBJLB53	261	1226988	1 - 2037	15 - 2051	
HBJNB52	262	1128792	1 - 793	15 - 807	
HDABQ83	263	1201703	1 - 446	15 - 460	
HDPDC84	264	1226990	1 - 3243	15 - 3257	
HDPUF40	265	1212494	1 - 2384	15 - 2398	
HDPWU07	266	1228286	1 - 3262	15 - 3276	
HDTJJ02	267	1106328	1 - 318	15 - 332	
HE2GA18	268	1121872	1 - 276	15 - 290	
HE2SY03	269	1207925	1 - 1070	15 - 1084	
HELGY64	270	1228289	1 - 2669	15 - 2683	
HFIYW31	271	1151476	1 - 1271	15 - 1285	
HFVIP88	272	1124705	1 - 898	15 - 912	
HGBAS76	273	1193040	1 - 1677	15 - 1691	
HHEBB62	274	1151481	1 - 541	15 - 555	
HHEHU73	275	1151483	1 - 1007	15 - 1021	
HHEMA11	276	1151484	1 - 638	15 - 652	
HHEQK01	277	1107392	1 - 622	15 - 636	
HHPEM84	278	915639	1 - 360	15 - 374	
HHSED84	279	1150832	1 - 760	15 - 774	
HIBCC94	280	1161292	1 - 1264	15 - 1278	

HKADN56	281	1220254	1 - 3121	15 - 3135	
HKIXG58	282	1124750	1 - 713	15 - 727	
HLICI13	283	1177963	1 - 1856	15 - 1870	
HLTGF17	284	662405	1 - 370	15 - 384	
HLYDC50	285	1151494	1 - 860	15 - 874	
HMADD49	286	1217031	1 - 2214	15 - 2228	
HMEKE78	287	1128290	1 - 1811	15 - 1825	
HMSHU26	288	1150833	1 - 1079	15 - 1093	
HNEEB82	289	1076509	1 - 677	15 - 691	
HNHIA06	290	1162086	1 - 710	15 - 724	
HODFY16	291	1105244	1 - 797	15 - 811	
HPQSB68	292	1221022	1 - 431	15 - 445	
HRDBH04	293	1150876	1 - 1472	15 - 1486	
HSICR69	294	1226965	1 - 1734	15 - 1748	
HSIGJ94	295	1105417	1 - 701	15 - 715	
HSYBL15	296	1104299	1 - 917	15 - 931	
HTEKH29	297	855660	1 - 2063	15 - 2077	
HTGEL46	298	1151520	1 - 1543	15 - 1557	
HTGFA05	299	1198110	1 - 1736	15 - 1750	
HTLDU61	300	1165319	1 - 1092	15 - 1106	
HTOFT34	301	1152490	1 - 1467	15 - 1481	
HTTDH46	302	1152491	1 - 1130	15 - 1144	
HTTIO05	303	1229905	1 - 2571	15 - 2585	
HWHGY45	304	911621	1 - 191	15 - 205	AC021102.
HWLQR48	305	1128304	1 - 494	15 - 508	
HWLQX76	306	1152280	1 - 453	15 - 467	
HATDD09	307	1165331	1 - 1282	15 - 1296	
HBJGT03	308	1105484	1 - 768	15 - 782	
HMTMF45	309	1141737	1 - 773	15 - 787	
HHPDV86	310	522953	1 - 666	15 - 680	AL109627, AL109627, AC025928, and AC025928.
HE8BT56	311	732602	1 - 365	15 - 379	
HUJDH06	312	907613	1 - 692	15 - 706	
HOEJG61	313	907614	1 - 660	15 - 674	
HE8PN24	314	907620	1 - 713	15 - 727	
HGBHI37	315	909745	1 - 491	15 - 505	
HCHOK82	316	909755	1 - 1077	15 - 1091	
HFPCH24	317	912608	1 - 474	15 - 488	
HTTKF86	318	912689	1 - 332	15 - 346	Z82188, Z82188, and Z82188.
HCESA79	319	912709	1 - 302	15 - 316	AC012171, AC012171, AC012171, AC009065, AC009065, AC009065, AC005346, AC005346, and AC005346.
HDTBJ28	320	912714	1 - 521	15 - 535	AP001793, AC008052, AC008052, AC015676, AC015676, and AP000864.
HDPBF48	321	912783	1 - 945	15 - 959	
HTPFY55	322	912928	1 - 562	15 - 576	
HMSCM47	323	923632	1 - 711	15 - 725	
HEOQA56	324	925132	1 - 413	15 - 427	AC013449.
HTPCQ24	325	925349	1 - 436	15 - 450	Z99716, and Z99716.
HWAEI37	326	929481	1 - 403	15 - 417	AL035461, and AL035461.
HDPSF03	327	969536	1 - 1283	15 - 1297	
HLHST63	328	581528	1 - 410	15 - 424	
HFAAJ44	329	489201	1 - 287	15 - 301	
HSLEM44	330	506604	1 - 337	15 - 351	AC078913, AC022123, and AC010357.
HETCL79	331	522826	1 - 465	15 - 479	
HFTAR20	332	670041	1 - 908	15 - 922	
HCUFD32	333	699379	1 - 702	15 - 716	

HKAEO39	334	705332	1 - 450	15 - 464	
HLWBR95	335	734474	1 - 908	15 - 922	AC013252, and AC013252.
HPWCJ63	336	772553	1 - 1407	15 - 1421	
HBXCM35	337	782911	1 - 578	15 - 592	
HULBN83	338	857836	1 - 624	15 - 638	
HAGET77	339	885265	1 - 1730	15 - 1744	
HMSOZ55	340	910911	1 - 979	15 - 993	AC024229, and AC024229.
HAPOR42	341	911292	1 - 1102	15 - 1116	
HMVAU10	342	911449	1 - 574	15 - 588	
HTTFY29	343	911454	1 - 707	15 - 721	
HHFJY06	344	911456	1 - 584	15 - 598	
HPCIK72	345	911459	1 - 269	15 - 283	
HFIDT84	346	919878	1 - 2655	15 - 2669	
HMCAV88	347	924874	1 - 1031	15 - 1045	AC068231, AC068231, AC068231, AL357752, AL357752, AC005476, and AC005476.
HKAIP73	348	928809	1 - 1441	15 - 1455	
HFVHV40	349	945849	1 - 668	15 - 682	AC020911, AC020911, and AC020911.
HTJN180	350	952231	1 - 1017	15 - 1031	
HEAAE08	351	959970	1 - 1053	15 - 1067	AC008687, and AC008687.
HDPLU91	352	963199	1 - 734	15 - 748	
HAPRM21	353	963200	1 - 857	15 - 871	AL034374, AL034374, and AL034374.
HTDAB30	354	965320	1 - 1248	15 - 1262	
H2CBN90	355	966919	1 - 809	15 - 823	
HETFJ47	356	971305	1 - 1767	15 - 1781	
HADEX52	357	971351	1 - 1819	15 - 1833	
HTADZ74	358	811489	1 - 602	15 - 616	AF077346, AC007278, and AC007278.
HAPNZ77	359	887072	1 - 469	15 - 483	AC003046, AC005859, AC076973, AC003046, AC005859, AC023098, and AC023098.
HELD74	360	963001	1 - 1414	15 - 1428	AI741422, AW249482, AA573909, AA085764, AW272801, AI052311, AA151131, AI700257, AA490620, AA310938, AI683396, AI284596, AA961817, AA862960, AW073675, R87485, AI828443, AI925221, AI969547, AW001375, N24896, AI521481, AI925228, AI695515, AA609182, AA151130, AI245859, AA490809, AA040451, AW139250, AI970384, AI961068, T67610, AA923298, AA513675, AW027490, T96070, AI624751, T67494, AI936161, AW196036, AA679554, AI917354, N36317, AA302588, AI932690, AW250249, R88163, T72363, AI796143, W32439, AA582049, AI539047, W45013, and AF113795.
HDPLJ22	361	859915	1 - 533	15 - 547	
HPMLD11	362	890204	1 - 1297	15 - 1311	
HMVDZ78	363	938574	1 - 236	15 - 250	AB002313.
HTSFJ40	364	722406	1 - 378	15 - 392	W28953, H19139, R54508, H10122, H08285, AA313257, R59784, F08505, R52605, Z43765, F08180, AI401170, F05493, F07194, R13670, R13641, Z45409, AW407594, F07185, AW407965, AA461135, AA371650, AC006171, AC006171, and AL161645.
HEMBZ62	365	742551	1 - 458	15 - 472	R13025.
HHFGZ38	366	785591	1 - 1153	15 - 1167	AA372117, AA133546, and AI468754.
HDPLN70	367	854010	1 - 968	15 - 982	

HSDJH12	368	876344	1 - 610	15 - 624	AA428452, AA134294, T83462, AI219740, AA010048, AI478566, AI990289, AC021747, AL359882, and AC046143.
HNBUT01	369	913838	1 - 1090	15 - 1104	AI219740, AI478566, AI632246, AA279757, AA977612, AA716656, AA687260, AI801069, AA071046, AI985849, AW370598, AA630617, AW370599, AW370625, AA134295, AW390691, AI990289, AA134294, AA428452, AI143764, D30955, AW370620, AA352142, AA074442, T83462, AW071043, T79236, and AI744728.
HEOQN14	370	923752	1 - 1031	15 - 1045	AI014538, AW006457, AI479414, AI805243, AI290929, AI129301, AI872459, AI601146, AI708870, AI973043, AI540074, AI186894, AI682389, AI654747, AA460832, AI392777, AA405714, AA649837, AI356090, AI358510, AW294364, AA954900, AA991687, AI540589, AI953865, AA977875, AW190678, R61326, R54477, AW009738, AA724308, AW297100, R54409, AA627570, AA504833, AA489470, H08185, R08582, AA778454, AI810108, Z41744, R43473, AA765208, AI698394, Z39824, H19140, Z41120, F03843, AA701889, AA159318, AW408231, AA404221, H84256, AW131981, AI401170, AA405779, AI475002, F01761, AW189730, H84262, F04422, AA404687, AA502309, AA371650, H29188, AA581151, AA477301, AA749407, AA477302, and AI144326.
HTXKL86	371	928194	1 - 767	15 - 781	AI810108, W28953, AA313257, AI401170, AW408231, AA371650, H19139, R54508, H10122, R59784, H08285, F08505, Z43765, AI014538, AA504833, R52605, F08180, AA765208, F05493, AA461135, F07194, R13641, AA701889, AA159318, Z45409, AW407594, H84256, AA404221, R13670, F07185, H84262, AA404687, AW407965, AI144326, AW006457, and AA581151.
HDQGV77	372	937546	1 - 1876	15 - 1890	
HE8TM80	373	955022	1 - 741	15 - 755	R56714, AA125853, AA127005, H06566, T70821, AA307834, H53723, and AF191018.
HWLEY40	374	957875	1 - 1443	15 - 1457	W28953, AI810108, AA159318, AA461135, H10122, AA313257, AA701889, AI654981, AI401170, H19139, H08285, AW408231, AA371650, R54508, R59784, AW407594, F07194, AA504833, F08180, F08505, Z43765, R52605, F07185, H84256, AW407965, F05493, H84262, AA404221, R13670, AA765208, Z45409, AA404687, R13641, AI014538, AI144326, AC006171, AC006171, and AL161645.
HDPPD36	375	493820	1 - 546	15 - 560	
HOUBZ94	376	527876	1 - 139	15 - 153	AC005954, AC005954, and AC068475.
HMIAH32	377	550977	1 - 689	15 - 703	
HDPHT43	378	573418	1 - 434	15 - 448	
HCE3W04	379	615501	1 - 859	15 - 873	AC025165, AC025165, AC022506, AC022506, and AC022366.
HMUBZ20	380	670393	1 - 349	15 - 363	

HDPAB51	381	685665	1 - 941	15 - 955	
HPJAP28	382	686349	1 - 432	15 - 446	AC004794, AC004794, and AC004794.
HIBEC79	383	703000	1 - 325	15 - 339	AC011458, AC011458, and AC011458.
HOQBF64	384	703177	1 - 389	15 - 403	
HTEDL38	385	761609	1 - 547	15 - 561	
HE9HI71	386	779375	1 - 668	15 - 682	
HNFHS82	387	779946	1 - 401	15 - 415	AC010835.
HOUHO89	388	786548	1 - 895	15 - 909	
HFPBB28	389	844526	1 - 321	15 - 335	AC016135, AC002518, AC073717, and AC018512.
HHEWQ61	390	876063	1 - 1052	15 - 1066	
HUFGH09	391	877078	1 - 635	15 - 649	
HLICA79	392	880881	1 - 2031	15 - 2045	
HSLIH01	393	884251	1 - 1868	15 - 1882	
HE9OV91	394	887364	1 - 774	15 - 788	
HHEDS85	395	894602	1 - 491	15 - 505	
HNTDJ68	396	899624	1 - 2389	15 - 2403	
HKAHO77	397	906671	1 - 699	15 - 713	
HTFNP84	398	909687	1 - 2474	15 - 2488	
HDQGZ78	399	909735	1 - 428	15 - 442	AC026282.
HHEMD52	400	909742	1 - 1605	15 - 1619	
HSIDQ38	401	909854	1 - 783	15 - 797	AC003070.
HSKBF02	402	909855	1 - 383	15 - 397	
HIBDE74	403	766011	1 - 508	15 - 522	
HWMAE53	404	909877	1 - 436	15 - 450	
HFXCG28	405	909961	1 - 596	15 - 610	
HFTCU45	406	910053	1 - 538	15 - 552	
HFTBL33	407	910055	1 - 1475	15 - 1489	AC025165, AC025165, and AC022366.
HTXJA84	408	911387	1 - 900	15 - 914	
HKAAW89	409	911389	1 - 433	15 - 447	
HSXDD55	410	911460	1 - 1164	15 - 1178	
HUFCI64	411	911558	1 - 759	15 - 773	AC004151, and AC004151.
HWAFT84	412	911559	1 - 1342	15 - 1356	AC004151, and AC004151.
HETCL18	413	914535	1 - 1388	15 - 1402	
HCRNK75	414	914536	1 - 2256	15 - 2270	
HTPFA03	415	922765	1 - 315	15 - 329	
HWADR60	416	926487	1 - 1275	15 - 1289	AC023176, and AC023176.
HWLFJ01	417	928017	1 - 781	15 - 795	
HTXNG95	418	928577	1 - 1380	15 - 1394	
HPCIG66	419	930886	1 - 945	15 - 959	AC024888, AC024888, and AC024888.
HCRPU72	420	931140	1 - 931	15 - 945	AC023151.
HE9RT95	421	934556	1 - 804	15 - 818	AC022420, AC022420, AC022420, and AC008439.
HFXJM13	422	935725	1 - 426	15 - 440	
HDPWU37	423	940705	1 - 522	15 - 536	
HHSDL85	424	942246	1 - 760	15 - 774	
HTJMD31	425	942848	1 - 638	15 - 652	
HWADD57	426	943039	1 - 996	15 - 1010	AC011492, and AC011492.
HLWAH05	427	944904	1 - 1338	15 - 1352	
HDPCI84	428	945527	1 - 2479	15 - 2493	
HBXDJ07	429	946830	1 - 1470	15 - 1484	H11405, R55569, N27906, H20863, N25140, and U27708.
HAMFD12	430	952438	1 - 526	15 - 540	
HFKHR40	431	952470	1 - 2240	15 - 2254	AC061707, AC061707, AC061707, AC018805, and AC018805.
HDTAI08	432	953265	1 - 590	15 - 604	
HMKCX80	433	956254	1 - 1174	15 - 1188	

HCEMF69	434	961308	1 - 1026	15 - 1040	
HWLHF10	435	963422	1 - 1387	15 - 1401	AC010545, AC010545, and AC010545.
HOEMG82	436	963855	1 - 1087	15 - 1101	
HFXDR37	437	965915	1 - 2442	15 - 2456	
HNNAS46	438	969470	1 - 1493	15 - 1507	
HRAAS26	439	971219	1 - 645	15 - 659	
HHEEL28	440	973096	1 - 524	15 - 538	
HCETF22	441	973324	1 - 2632	15 - 2646	
HCMSF55	442	912284	1 - 715	15 - 729	

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TABLE 4

Code	Description	Tissue	Organ	Cell Line	Disease	Vector
AR022	a_Heart	a_Heart				
AR023	a_Liver	a_Liver				
AR024	a_mammary gland	a_mammary gland				
AR025	a_Prostate	a_Prostate				
AR026	a_small intestine	a_small intestine				
AR027	a_Stomach	a_Stomach				
AR028	Blood B cells	Blood B cells				
AR029	Blood B cells activated	Blood B cells activated				
AR030	Blood B cells resting	Blood B cells resting				
AR031	Blood T cells activated	Blood T cells activated				
AR032	Blood T cells resting	Blood T cells resting				
AR033	brain	brain				
AR034	breast	breast				
AR035	breast cancer	breast cancer				
AR036	Cell Line CAOV3	Cell Line CAOV3				
AR037	cell line PA-1	cell line PA-1				
AR038	cell line transformed	cell line transformed				
AR039	colon	colon				
AR040	colon (9808co65R)	colon (9808co65R)				
AR041	colon (9809co15)	colon (9809co15)				
AR042	colon cancer	colon cancer				
AR043	colon cancer (9808co64R)	colon cancer (9808co64R)				
AR044	colon cancer 9809co14	colon cancer 9809co14				
AR045	corn clone 5	corn clone 5				
AR046	corn clone 6	corn clone 6				
AR047	corn clone2	corn clone2				
AR048	corn clone3	corn clone3				
AR049	Corn Clone4	Corn Clone4				
AR050	Donor II B Cells 24hrs	Donor II B Cells 24hrs				
AR051	Donor II B Cells 72hrs	Donor II B Cells 72hrs				
AR052	Donor II B-Cells 24 hrs.	Donor II B-Cells 24 hrs.				
AR053	Donor II B-Cells 72hrs	Donor II B-Cells 72hrs				
AR054	Donor II Resting B Cells	Donor II Resting B Cells				
AR055	Heart	Heart				
AR056	Human Lung (clonotech)	Human Lung (clonotech)				
AR057	Human Mammary (clontech)	Human Mammary (clontech)				

AR058	Human Thymus (clonotech)	Human Thymus (clonotech)				
AR059	Jurkat (unstimulated)	Jurkat (unstimulated)				
AR060	Kidney	Kidney				
AR061	Liver	Liver				
AR062	Liver (Clontech)	Liver (Clontech)				
AR063	Lymphocytes chronic lymphocytic leukaemia	Lymphocytes chronic lymphocytic leukaemia				
AR064	Lymphocytes diffuse large B cell lymphoma	Lymphocytes diffuse large B cell lymphoma				
AR065	Lymphocytes follicular lymphoma	Lymphocytes follicular lymphoma				
AR066	normal breast	normal breast				
AR067	Normal Ovarian (4004901)	Normal Ovarian (4004901)				
AR068	Normal Ovary 9508G045	Normal Ovary 9508G045				
AR069	Normal Ovary 9701G208	Normal Ovary 9701G208				
AR070	Normal Ovary 9806G005	Normal Ovary 9806G005				
AR071	Ovarian Cancer	Ovarian Cancer				
AR072	Ovarian Cancer (9702G001)	Ovarian Cancer (9702G001)				
AR073	Ovarian Cancer (9707G029)	Ovarian Cancer (9707G029)				
AR074	Ovarian Cancer (9804G011)	Ovarian Cancer (9804G011)				
AR075	Ovarian Cancer (9806G019)	Ovarian Cancer (9806G019)				
AR076	Ovarian Cancer (9807G017)	Ovarian Cancer (9807G017)				
AR077	Ovarian Cancer (9809G001)	Ovarian Cancer (9809G001)				
AR078	ovarian cancer 15799	ovarian cancer 15799				
AR079	Ovarian Cancer 17717A1D	Ovarian Cancer 17717A1D				
AR080	Ovarian Cancer 4004664B1	Ovarian Cancer 4004664B1				
AR081	Ovarian Cancer 4005315A1	Ovarian Cancer 4005315A1				
AR082	ovarian cancer 94127303	ovarian cancer 94127303				
AR083	Ovarian Cancer 96069304	Ovarian Cancer 96069304				
AR084	Ovarian Cancer 9707G029	Ovarian Cancer 9707G029				
AR085	Ovarian Cancer 9807G045	Ovarian Cancer 9807G045				

AR086	ovarian cancer 9809G001	ovarian cancer 9809G001				
AR087	Ovarian Cancer 9905C032RC	Ovarian Cancer 9905C032RC				
AR088	Ovarian cancer 9907 C00 3rd	Ovarian cancer 9907 C00 3rd				
AR089	Prostate	Prostate				
AR090	Prostate (clonotech)	Prostate (clonotech)				
AR091	prostate cancer	prostate cancer				
AR092	prostate cancer #15176	prostate cancer #15176				
AR093	prostate cancer #15509	prostate cancer #15509				
AR094	prostate cancer #15673	prostate cancer #15673				
AR095	Small Intestine (Clontech)	Small Intestine (Clontech)				
AR096	Spleen	Spleen				
AR097	Thymus T cells activated	Thymus T cells activated				
AR098	Thymus T cells resting	Thymus T cells resting				
AR099	Tonsil	Tonsil				
AR100	Tonsil germinal center centroblast	Tonsil germinal center centroblast				
AR101	Tonsil germinal center B cell	Tonsil germinal center B cell				
AR102	Tonsil lymph node	Tonsil lymph node				
AR103	Tonsil memory B cell	Tonsil memory B cell				
AR104	Whole Brain	Whole Brain				
AR105	Xenograft ES-2	Xenograft ES-2				
AR106	Xenograft SW626	Xenograft SW626				
H0002	Human Adult Heart	Human Adult Heart	Heart			Uni-ZAP XR
H0004	Human Adult Spleen	Human Adult Spleen	Spleen			Uni-ZAP XR
H0008	Whole 6 Week Old Embryo					Uni-ZAP XR
H0009	Human Fetal Brain					Uni-ZAP XR
H0011	Human Fetal Kidney	Human Fetal Kidney	Kidney			Uni-ZAP XR
H0012	Human Fetal Kidney	Human Fetal Kidney	Kidney			Uni-ZAP XR
H0013	Human 8 Week Whole Embryo	Human 8 Week Old Embryo	Embryo			Uni-ZAP XR
H0014	Human Gall Bladder	Human Gall Bladder	Gall Bladder			Uni-ZAP XR
H0015	Human Gall Bladder, fraction II	Human Gall Bladder	Gall Bladder			Uni-ZAP XR
H0022	Jurkat Cells	Jurkat T-Cell Line				Lambda ZAP II
H0023	Human Fetal Lung					Uni-ZAP XR
H0024	Human Fetal Lung III	Human Fetal Lung	Lung			Uni-ZAP XR
H0025	Human Adult Lymph Node	Human Adult Lymph Node	Lymph Node			Lambda ZAP II
H0026	Namalwa Cells	Namalwa B-Cell				Lambda ZAP II

		Line, EBV immortalized				
H0027	Human Ovarian Cancer				disease	Uni-ZAP XR
H0028	Human Old Ovary	Human Old Ovary	Ovary			pBluescript
H0029	Human Pancreas	Human Pancreas	Pancreas			Uni-ZAP XR
H0030	Human Placenta					Uni-ZAP XR
H0031	Human Placenta	Human Placenta	Placenta			Uni-ZAP XR
H0032	Human Prostate	Human Prostate	Prostate			Uni-ZAP XR
H0033	Human Pituitary	Human Pituitary				Uni-ZAP XR
H0036	Human Adult Small Intestine	Human Adult Small Intestine	Small Int.			Uni-ZAP XR
H0037	Human Adult Small Intestine	Human Adult Small Intestine	Small Int.			pBluescript
H0038	Human Testes	Human Testes	Testis			Uni-ZAP XR
H0039	Human Pancreas Tumor	Human Pancreas Tumor	Pancreas		disease	Uni-ZAP XR
H0040	Human Testes Tumor	Human Testes Tumor	Testis		disease	Uni-ZAP XR
H0041	Human Fetal Bone	Human Fetal Bone	Bone			Uni-ZAP XR
H0042	Human Adult Pulmonary	Human Adult Pulmonary	Lung			Uni-ZAP XR
H0046	Human Endometrial Tumor	Human Endometrial Tumor	Uterus		disease	Uni-ZAP XR
H0050	Human Fetal Heart	Human Fetal Heart	Heart			Uni-ZAP XR
H0051	Human Hippocampus	Human Hippocampus	Brain			Uni-ZAP XR
H0052	Human Cerebellum	Human Cerebellum	Brain			Uni-ZAP XR
H0056	Human Umbilical Vein, Endo. remake	Human Umbilical Vein Endothelial Cells	Umbilical vein			Uni-ZAP XR
H0057	Human Fetal Spleen					Uni-ZAP XR
H0059	Human Uterine Cancer	Human Uterine Cancer	Uterus		disease	Lambda ZAP II
H0063	Human Thymus	Human Thymus	Thymus			Uni-ZAP XR
H0064	Human Right Hemisphere of Brain	Human Brain, right hemisphere	Brain			Uni-ZAP XR
H0068	Human Skin Tumor	Human Skin Tumor	Skin		disease	Uni-ZAP XR
H0069	Human Activated T-Cells	Activated T-Cells	Blood	Cell Line		Uni-ZAP XR
H0071	Human Infant Adrenal Gland	Human Infant Adrenal Gland	Adrenal gland			Uni-ZAP XR
H0075	Human Activated T-Cells (II)	Activated T-Cells	Blood	Cell Line		Uni-ZAP XR
H0079	Human Whole 7 Week Old Embryo (II)	Human Whole 7 Week Old Embryo	Embryo			Uni-ZAP XR
H0081	Human Fetal Epithelium (Skin)	Human Fetal Skin	Skin			Uni-ZAP XR
H0082	Human Fetal Muscle	Human Fetal Muscle	Sk Muscle			Uni-ZAP XR
H0083	HUMAN JURKAT MEMBRANE BOUND POLYSOMES	Jurkat Cells				Uni-ZAP XR
H0085	Human Colon	Human Colon				Lambda ZAP II
H0086	Human epithelioid	Epithelioid	Sk Muscle		disease	Uni-ZAP XR

	sarcoma	Sarcoma, muscle				
H0087	Human Thymus	Human Thymus				pBluescript
H0090	Human T-Cell Lymphoma	T-Cell Lymphoma	T-Cell		disease	Uni-ZAP XR
H0092	Human Pancreas Tumor	Human Pancreas Tumor	Pancreas		disease	Uni-ZAP XR
H0098	Human Adult Liver, subtracted	Human Adult Liver	Liver			Uni-ZAP XR
H0100	Human Whole Six Week Old Embryo	Human Whole Six Week Old Embryo	Embryo			Uni-ZAP XR
H0101	Human 7 Weeks Old Embryo, subtracted	Human Whole 7 Week Old Embryo	Embryo			Lambda ZAP II
H0102	Human Whole 6 Week Old Embryo (II), subt	Human Whole Six Week Old Embryo	Embryo			pBluescript
H0105	Human Fetal Heart, subtracted	Human Fetal Heart	Heart			pBluescript
H0107	Human Infant Adrenal Gland, subtracted	Human Infant Adrenal Gland	Adrenal gland			pBluescript
H0108	Human Adult Lymph Node, subtracted	Human Adult Lymph Node	Lymph Node			Uni-ZAP XR
H0111	Human Placenta, subtracted	Human Placenta	Placenta			pBluescript
H0112	Human Parathyroid Tumor, subtracted	Human Parathyroid Tumor	Parathyroid			pBluescript
H0118	Human Adult Kidney	Human Adult Kidney	Kidney			Uni-ZAP XR
H0122	Human Adult Skeletal Muscle	Human Skeletal Muscle	Sk Muscle			Uni-ZAP XR
H0123	Human Fetal Dura Mater	Human Fetal Dura Mater	Brain			Uni-ZAP XR
H0124	Human Rhabdomyosarcoma	Human Rhabdomyosarcoma	Sk Muscle		disease	Uni-ZAP XR
H0125	Cem cells cyclohexamide treated	Cyclohexamide Treated Cem, Jurkat, Raji, and Supt	Blood	Cell Line		Uni-ZAP XR
H0130	LNCAP untreated	LNCAP Cell Line	Prostate	Cell Line		Uni-ZAP XR
H0131	LNCAP + 0.3nM R1881	LNCAP Cell Line	Prostate	Cell Line		Uni-ZAP XR
H0132	LNCAP + 30nM R1881	LNCAP Cell Line	Prostate	Cell Line		Uni-ZAP XR
H0134	Raji Cells, cyclohexamide treated	Cyclohexamide Treated Cem, Jurkat, Raji, and Supt	Blood	Cell Line		Uni-ZAP XR
H0135	Human Synovial Sarcoma	Human Synovial Sarcoma	Synovium			Uni-ZAP XR
H0136	Supt Cells, cyclohexamide treated	Cyclohexamide Treated Cem, Jurkat, Raji, and Supt	Blood	Cell Line		Uni-ZAP XR
H0140	Activated T-Cells, 8 hrs.	Activated T-Cells	Blood	Cell Line		Uni-ZAP XR
H0144	Nine Week Old Early Stage Human	9 Wk Old Early Stage Human	Embryo			Uni-ZAP XR
H0149	7 Week Old Early Stage Human, subtracted	Human Whole 7 Week Old Embryo	Embryo			Uni-ZAP XR
H0150	Human Epididymus	Epididymis	Testis			Uni-ZAP XR
H0152	Early Stage Human Liver, fract (II)	Human Fetal Liver	Liver			Uni-ZAP XR

H0154	Human Fibrosarcoma	Human Skin Fibrosarcoma	Skin		disease	Uni-ZAP XR
H0156	Human Adrenal Gland Tumor	Human Adrenal Gland Tumor	Adrenal Gland		disease	Uni-ZAP XR
H0159	Activated T-Cells, 8 hrs., ligation 2	Activated T-Cells	Blood	Cell Line		Uni-ZAP XR
H0161	Activated T-Cells, 24 hrs., ligation 2	Activated T-Cells	Blood	Cell Line		Uni-ZAP XR
H0163	Human Synovium	Human Synovium	Synovium			Uni-ZAP XR
H0165	Human Prostate Cancer, Stage B2	Human Prostate Cancer, stage B2	Prostate		disease	Uni-ZAP XR
H0166	Human Prostate Cancer, Stage B2 fraction	Human Prostate Cancer, stage B2	Prostate		disease	Uni-ZAP XR
H0169	Human Prostate Cancer, Stage C fraction	Human Prostate Cancer, stage C	Prostate		disease	Uni-ZAP XR
H0170	12 Week Old Early Stage Human	Twelve Week Old Early Stage Human	Embryo			Uni-ZAP XR
H0171	12 Week Old Early Stage Human, II	Twelve Week Old Early Stage Human	Embryo			Uni-ZAP XR
H0172	Human Fetal Brain, random primed	Human Fetal Brain	Brain			Lambda ZAP II
H0175	H. Adult Spleen, ziplox					pSport1
H0177	CAMA1Ee Cell Line	CAMA1Ee Cell Line	Breast	Cell Line		Uni-ZAP XR
H0178	Human Fetal Brain	Human Fetal Brain	Brain			Uni-ZAP XR
H0179	Human Neutrophil	Human Neutrophil	Blood	Cell Line		Uni-ZAP XR
H0180	Human Primary Breast Cancer	Human Primary Breast Cancer	Breast		disease	Uni-ZAP XR
H0181	Human Primary Breast Cancer	Human Primary Breast Cancer	Breast		disease	Uni-ZAP XR
H0182	Human Primary Breast Cancer	Human Primary Breast Cancer	Breast		disease	Uni-ZAP XR
H0187	Resting T-Cell	T-Cells	Blood	Cell Line		Lambda ZAP II
H0188	Human Normal Breast	Human Normal Breast	Breast			Uni-ZAP XR
H0189	Human Resting Macrophage	Human Macrophage/Monocytes	Blood	Cell Line		Uni-ZAP XR
H0191	Human Activated Macrophage (LPS), thiour	Human Macrophage/Monocytes	Blood	Cell Line		Uni-ZAP XR
H0194	Human Cerebellum, subtracted	Human Cerebellum	Brain			pBluescript
H0196	Human Cardiomyopathy, subtracted	Human Cardiomyopathy	Heart			Uni-ZAP XR
H0197	Human Fetal Liver, subtracted	Human Fetal Liver	Liver			Uni-ZAP XR
H0199	Human Fetal Liver, subtracted, neg clone	Human Fetal Liver	Liver			Uni-ZAP XR
H0201	Human Hippocampus, subtracted	Human Hippocampus	Brain			pBluescript
H0208	Early Stage Human Lung, subtracted	Human Fetal Lung	Lung			pBluescript

H0212	Human Prostate, subtracted	Human Prostate	Prostate			pBluescript
H0213	Human Pituitary, subtracted	Human Pituitary				Uni-ZAP XR
H0216	Supt cells, cyclohexamide treated, subtracted	Cyclohexamide Treated Cem, Jurkat, Raji, and Supt	Blood	Cell Line		pBluescript
H0217	Supt cells, cyclohexamide treated, differentially expressed	Cyclohexamide Treated Cem, Jurkat, Raji, and Supt	Blood	Cell Line		pBluescript
H0222	Activated T-Cells, 8 hrs, subtracted	Activated T-Cells	Blood	Cell Line		Uni-ZAP XR
H0231	Human Colon, subtraction	Human Colon				pBluescript
H0233	Human Fetal Heart, Differential (Adult-Specific)	Human Fetal Heart	Heart			pBluescript
H0234	human colon cancer, metastatic to liver, differentially expressed	Human Colon Cancer, metasticized to liver	Liver			pBluescript
H0235	Human colon cancer, metaticized to liver, subtraction	Human Colon Cancer, metasticized to liver	Liver			pBluescript
H0239	Human Kidney Tumor	Human Kidney Tumor	Kidney		disease	Uni-ZAP XR
H0241	C7MCF7 cell line, estrogen treated, subtraction	C7MCF7 Cell Line, estrogen treated	Breast	Cell Line		Uni-ZAP XR
H0244	Human 8 Week Whole Embryo, subtracted	Human 8 Week Old Embryo	Embryo			Uni-ZAP XR
H0246	Human Fetal Liver-Enzyme subtraction	Human Fetal Liver	Liver			Uni-ZAP XR
H0247	Human Membrane Bound Polysomes- Enzyme Subtraction	Human Membrane Bound Polysomes	Blood	Cell Line		Uni-ZAP XR
H0249	HE7, subtracted by hybridization with E7 cDNA	Human Whole 7 Week Old Embryo	Embryo			Uni-ZAP XR
H0250	Human Activated Monocytes	Human Monocytes				Uni-ZAP XR
H0251	Human Chondrosarcoma	Human Chondrosarcoma	Cartilage		disease	Uni-ZAP XR
H0252	Human Osteosarcoma	Human Osteosarcoma	Bone		disease	Uni-ZAP XR
H0253	Human adult testis, large inserts	Human Adult Testis	Testis			Uni-ZAP XR
H0254	Breast Lymph node cDNA library	Breast Lymph Node	Lymph Node			Uni-ZAP XR
H0255	breast lymph node CDNA library	Breast Lymph Node	Lymph Node			Lambda ZAP II
H0257	HL-60, PMA 4H	HL-60 Cells, PMA stimulated 4H	Blood	Cell Line		Uni-ZAP XR
H0261	H. cerebellum, Enzyme subtracted	Human Cerebellum	Brain			Uni-ZAP XR

H0263	human colon cancer	Human Colon Cancer	Colon		disease	Lambda ZAP II
H0264	human tonsils	Human Tonsil	Tonsil			Uni-ZAP XR
H0265	Activated T-Cell (12hs)/Thiouridine labelledEco	T-Cells	Blood	Cell Line		Uni-ZAP XR
H0266	Human Microvascular Endothelial Cells, fract. A	HMEC	Vein	Cell Line		Lambda ZAP II
H0267	Human Microvascular Endothelial Cells, fract. B	HMEC	Vein	Cell Line		Lambda ZAP II
H0268	Human Umbilical Vein Endothelial Cells, fract. A	HUVE Cells	Umbilical vein	Cell Line		Lambda ZAP II
H0269	Human Umbilical Vein Endothelial Cells, fract. B	HUVE Cells	Umbilical vein	Cell Line		Lambda ZAP II
H0271	Human Neutrophil, Activated	Human Neutrophil - Activated	Blood	Cell Line		Uni-ZAP XR
H0272	HUMAN TONSILS, FRACTION 2	Human Tonsil	Tonsil			Uni-ZAP XR
H0280	K562 + PMA (36 hrs)	K562 Cell line	cell line	Cell Line		ZAP Express
H0282	HBGB's differential consolidation	Human Primary Breast Cancer	Breast			Uni-ZAP XR
H0284	Human OB MG63 control fraction I	Human Osteoblastoma MG63 cell line	Bone	Cell Line		Uni-ZAP XR
H0286	Human OB MG63 treated (10 nM E2) fraction I	Human Osteoblastoma MG63 cell line	Bone	Cell Line		Uni-ZAP XR
H0288	Human OB HOS control fraction I	Human Osteoblastoma HOS cell line	Bone	Cell Line		Uni-ZAP XR
H0290	Human OB HOS treated (1 nM E2) fraction I	Human Osteoblastoma HOS cell line	Bone	Cell Line		Uni-ZAP XR
H0292	Human OB HOS treated (10 nM E2) fraction I	Human Osteoblastoma HOS cell line	Bone	Cell Line		Uni-ZAP XR
H0294	Amniotic Cells - TNF induced	Amniotic Cells - TNF induced	Placenta	Cell Line		Uni-ZAP XR
H0295	Amniotic Cells - Primary Culture	Amniotic Cells - Primary Culture	Placenta	Cell Line		Uni-ZAP XR
H0298	HCB'B's differential consolidation	CAMA1Ee Cell Line	Breast	Cell Line		Uni-ZAP XR
H0299	HCBA's differential consolidation	CAMA1Ee Cell Line	Breast	Cell Line		Uni-ZAP XR
H0300	CD34 positive cells (Cord Blood)	CD34 Positive Cells	Cord Blood			ZAP Express
H0305	CD34 positive cells (Cord Blood)	CD34 Positive Cells	Cord Blood			ZAP Express
H0306	CD34 depleted Buffy Coat (Cord Blood)	CD34 Depleted Buffy Coat (Cord Blood)	Cord Blood			ZAP Express
H0309	Human Chronic Synovitis	Synovium, Chronic Synovitis/	Synovium		disease	Uni-ZAP XR

		Osteoarthritis				
H0310	human caudate nucleus	Brain	Brain			Uni-ZAP XR
H0316	HUMAN STOMACH	Human Stomach	Stomach			Uni-ZAP XR
H0318	HUMAN B CELL LYMPHOMA	Human B Cell Lymphoma	Lymph Node		disease	Uni-ZAP XR
H0320	Human frontal cortex	Human Frontal Cortex	Brain			Uni-ZAP XR
H0327	human corpus colosum	Human Corpus Callosum	Brain			Uni-ZAP XR
H0328	human ovarian cancer	Ovarian Cancer	Ovary		disease	Uni-ZAP XR
H0329	Dermatofibrosarcoma Protuberance	Dermatofibrosarcoma Protuberans	Skin		disease	Uni-ZAP XR
H0331	Hepatocellular Tumor	Hepatocellular Tumor	Liver		disease	Lambda ZAP II
H0333	Hemangiopericytoma	Hemangiopericytoma	Blood vessel		disease	Lambda ZAP II
H0334	Kidney cancer	Kidney Cancer	Kidney		disease	Uni-ZAP XR
H0339	Duodenum	Duodenum				Uni-ZAP XR
H0340	Corpus Callosum	Corpus Collosum-93052				Uni-ZAP XR
H0341	Bone Marrow Cell Line (RS4;11)	Bone Marrow Cell Line RS4;11	Bone Marrow	Cell Line		Uni-ZAP XR
H0342	Lingual Gyrus	Lingual Gyrus	Brain			Uni-Zap XR
H0343	stomach cancer (human)	Stomach Cancer - 5383A (human)			disease	Uni-ZAP XR
H0345	SKIN	Skin - 4000868H	Skin			Uni-ZAP XR
H0349	human adult liver cDNA library	Human Adult Liver	Liver			pCMVSPORT 1
H0351	Glioblastoma	Glioblastoma	Brain		disease	Uni-ZAP XR
H0352	wilm's tumor	Wilm's Tumor			disease	Uni-ZAP XR
H0355	Human Liver	Human Liver, normal Adult				pCMVSPORT 1
H0356	Human Kidney	Human Kidney	Kidney			pCMVSPORT 1
H0359	KMH2 cell line	KMH2				ZAP Express
H0361	Human rejected kidney	Human Rejected Kidney			disease	pBluescript
H0364	Human Osteoclastoma, excised	Human Osteoclastoma			disease	pBluescript
H0365	Osteoclastoma-normalized B	Human Osteoclastoma			disease	Uni-ZAP XR
H0366	L428 cell line	L428				ZAP Express
H0369	H. Atrophic Endometrium	Atrophic Endometrium and myometrium				Uni-ZAP XR
H0370	H. Lymph node breast Cancer	Lymph node with Met. Breast Cancer			disease	Uni-ZAP XR
H0372	Human Testes	Human Testes	Testis			pCMVSPORT 1
H0373	Human Heart	Human Adult Heart	Heart			pCMVSPORT 1
H0374	Human Brain	Human Brain				pCMVSPORT 1
H0375	Human Lung	Human Lung				pCMVSPORT 1
H0376	Human Spleen	Human Adult Spleen	Spleen			pCMVSPORT 1

H0379	Human Tongue, frac I	Human Tongue				pSport1
H0381	Bone Cancer	Bone Cancer			disease	Uni-ZAP XR
H0383	Human Prostate BPH, re-excision	Human Prostate BPH				Uni-ZAP XR
H0384	Brain, Kozak	Human Brain				pCMVSPORT 1
H0386	Leukocyte and Lung; 4 screens	Human Leukocytes	Blood	Cell Line		pCMVSPORT 1
H0388	Human Rejected Kidney, 704 re-excision	Human Rejected Kidney			disease	pBluescript
H0390	Human Amygdala Depression, re-excision	Human Amygdala Depression			disease	pBluescript
H0391	H. Meningioma, M6	Human Meningioma	brain			pSport1
H0392	H. Meningioma, M1	Human Meningioma	brain			pSport1
H0393	Fetal Liver, subtraction II	Human Fetal Liver	Liver			pBluescript
H0394	A-14 cell line	Redd-Sternberg cell				ZAP Express
H0395	A1-CELL LINE	Redd-Sternberg cell				ZAP Express
H0396	L1 Cell line	Redd-Sternberg cell				ZAP Express
H0399	Human Kidney Cortex, re-rescue	Human Kidney Cortex				Lambda ZAP II
H0400	Human Striatum Depression, re-rescue	Human Brain, Striatum Depression	Brain			Lambda ZAP II
H0401	Human Pituitary, subtracted V	Human Pituitary				pBluescript
H0402	CD34 depleted Buffy Coat (Cord Blood), re-excision	CD34 Depleted Buffy Coat (Cord Blood)	Cord Blood			ZAP Express
H0408	Human kidney Cortex, subtracted	Human Kidney Cortex				pBluescript
H0409	H. Striatum Depression, subtracted	Human Brain, Striatum Depression	Brain			pBluescript
H0411	H Female Bladder, Adult	Human Female Adult Bladder	Bladder			pSport1
H0412	Human umbilical vein endothelial cells, IL-4 induced	HUVE Cells	Umbilical vein	Cell Line		pSport1
H0413	Human Umbilical Vein Endothelial Cells, uninduced	HUVE Cells	Umbilical vein	Cell Line		pSport1
H0414	Ovarian Tumor I, OV5232	Ovarian Tumor, OV5232	Ovary		disease	pSport1
H0415	H. Ovarian Tumor, II, OV5232	Ovarian Tumor, OV5232	Ovary		disease	pCMVSPORT 2.0
H0416	Human Neutrophils, Activated, re-excision	Human Neutrophil - Activated	Blood	Cell Line		pBluescript
H0417	Human Pituitary, subtracted VIII	Human Pituitary				pBluescript
H0421	Human Bone Marrow, re-excision	Bone Marrow				pBluescript
H0422	T-Cell PHA 16 hrs	T-Cells	Blood	Cell Line		pSport1
H0423	T-Cell PHA 24 hrs	T-Cells	Blood	Cell Line		pSport1
H0424	Human Pituitary, subt IX	Human Pituitary				pBluescript
H0427	Human Adipose	Human Adipose, left hiplipoma				pSport1

H0428	Human Ovary	Human Ovary Tumor	Ovary			pSport1
H0429	K562 + PMA (36 hrs),re-excision	K562 Cell line	cell line	Cell Line		ZAP Express
H0431	H. Kidney Medulla, re-excision	Kidney medulla	Kidney			pBluescript
H0433	Human Umbilical Vein Endothelial cells, frac B, re-excision	HUVE Cells	Umbilical vein	Cell Line		pBluescript
H0434	Human Brain, striatum, re-excision	Human Brain, Striatum				pBluescript
H0435	Ovarian Tumor 10-3-95	Ovarian Tumor, OV350721	Ovary			pCMVSPORT 2.0
H0436	Resting T-Cell Library,II	T-Cells	Blood	Cell Line		pSport1
H0437	H Umbilical Vein Endothelial Cells, frac A, re-excision	HUVE Cells	Umbilical vein	Cell Line		Lambda ZAP II
H0438	H. Whole Brain #2, re-excision	Human Whole Brain #2				ZAP Express
H0441	H. Kidney Cortex, subtracted	Kidney cortex	Kidney			pBluescript
H0443	H. Adipose, subtracted	Human Adipose, left hiplipoma				pSport1
H0444	Spleen metastatic melanoma	Spleen, Metastatic malignant melanoma	Spleen		disease	pSport1
H0445	Spleen, Chronic lymphocytic leukemia	Human Spleen, CLL	Spleen		disease	pSport1
H0453	H. Kidney Pyramid, subtracted	Kidney pyramids	Kidney			pBluescript
H0455	H. Striatum Depression, subt	Human Brain, Striatum Depression	Brain			pBluescript
H0457	Human Eosinophils	Human Eosinophils				pSport1
H0458	CD34+ cell, I, frac II	CD34 positive cells				pSport1
H0459	CD34+cells, II, FRACTION 2	CD34 positive cells				pCMVSPORT 2.0
H0462	H. Amygdala Depression, subtracted		Brain			pBluescript
H0477	Human Tonsil, Lib 3	Human Tonsil	Tonsil			pSport1
H0478	Salivary Gland, Lib 2	Human Salivary Gland	Salivary gland			pSport1
H0479	Salivary Gland, Lib 3	Human Salivary Gland	Salivary gland			pSport1
H0483	Breast Cancer cell line, MDA 36	Breast Cancer Cell line, MDA 36				pSport1
H0484	Breast Cancer Cell line, angiogenic	Breast Cancer Cell line, Angiogenic, 36T3				pSport1
H0485	Hodgkin's Lymphoma I	Hodgkin's Lymphoma I			disease	pCMVSPORT 2.0
H0486	Hodgkin's Lymphoma II	Hodgkin's Lymphoma II			disease	pCMVSPORT 2.0
H0487	Human Tonsils, lib I	Human Tonsils				pCMVSPORT 2.0

H0488	Human Tonsils, Lib 2	Human Tonsils				pCMVSPORT 2.0
H0489	Crohn's Disease	Ileum	Intestine		disease	pSport1
H0492	HL-60, RA 4h, Subtracted	HL-60 Cells, RA stimulated for 4H	Blood	Cell Line		Uni-ZAP XR
H0494	Keratinocyte	Keratinocyte				pCMVSPORT 2.0
H0497	HEL cell line	HEL cell line		HEL 92.1.7		pSport1
H0505	Human Astrocyte	Human Astrocyte				pSport1
H0506	Ulcerative Colitis	Colon	Colon			pSport1
H0509	Liver, Hepatoma	Human Liver, Hepatoma, patient 8	Liver		disease	pCMVSPORT 3.0
H0510	Human Liver, normal	Human Liver, normal, Patient # 8	Liver			pCMVSPORT 3.0
H0517	Nasal polyps	Nasal polyps				pCMVSPORT 2.0
H0518	pBMC stimulated w/ poly I/C	pBMC stimulated with poly I/C				pCMVSPORT 3.0
H0519	NTERA2, control	NTERA2, Teratocarcinoma cell line				pCMVSPORT 3.0
H0520	NTERA2 + retinoic acid, 14 days	NTERA2, Teratocarcinoma cell line				pSport1
H0521	Primary Dendritic Cells, lib 1	Primary Dendritic cells				pCMVSPORT 3.0
H0522	Primary Dendritic cells, frac 2	Primary Dendritic cells				pCMVSPORT 3.0
H0525	PCR, pBMC I/C treated	pBMC stimulated with poly I/C				PCR11
H0528	Poly[I]/Poly[C] Normal Lung Fibroblasts	Poly[I]/Poly[C] Normal Lung Fibroblasts				pCMVSPORT 3.0
H0529	Myeloid Progenitor Cell Line	TF-1 Cell Line; Myeloid progenitor cell line				pCMVSPORT 3.0
H0530	Human Dermal Endothelial Cells, untreated	Human Dermal Endothelial Cells; untreated				pSport1
H0538	Merkel Cells	Merkel cells	Lymph node			pSport1
H0539	Pancreas Islet Cell Tumor	Pancreas Islet Cell Tumour	Pancreas		disease	pSport1
H0540	Skin, burned	Skin, leg burned	Skin			pSport1
H0542	T Cell helper I	Helper T cell				pCMVSPORT 3.0
H0543	T cell helper II	Helper T cell				pCMVSPORT 3.0
H0544	Human endometrial stromal cells	Human endometrial stromal cells				pCMVSPORT 3.0
H0545	Human endometrial stromal cells-treated with progesterone	Human endometrial stromal cells-treated with proge				pCMVSPORT 3.0
H0546	Human endometrial stromal cells-treated with estradiol	Human endometrial stromal cells-treated with estra				pCMVSPORT 3.0
H0547	NTERA2 teratocarcinoma cell line+retinoic acid (14	NTERA2, Teratocarcinoma				pSport1

	days)	cell line				
H0549	H. Epididymus, caput & corpus	Human Epididymus, caput and corpus				Uni-ZAP XR
H0550	H. Epididymus, cauda	Human Epididymus, cauda				Uni-ZAP XR
H0551	Human Thymus Stromal Cells	Human Thymus Stromal Cells				pCMVSPORT 3.0
H0553	Human Placenta	Human Placenta				pCMVSPORT 3.0
H0555	Rejected Kidney, lib 4	Human Rejected Kidney	Kidney		disease	pCMVSPORT 3.0
H0556	Activated T-cell(12h)/Thiouridine-re-excision	T-Cells	Blood	Cell Line		Uni-ZAP XR
H0559	HL-60, PMA 4H, re-excision	HL-60 Cells, PMA stimulated 4H	Blood	Cell Line		Uni-ZAP XR
H0560	KMH2	KMH2				pCMVSPORT 3.0
H0561	L428	L428				pCMVSPORT 3.0
H0562	Human Fetal Brain, normalized c5-11-26	Human Fetal Brain				pCMVSPORT 2.0
H0563	Human Fetal Brain, normalized 50021F	Human Fetal Brain				pCMVSPORT 2.0
H0566	Human Fetal Brain,normalized c50F	Human Fetal Brain				pCMVSPORT 2.0
H0569	Human Fetal Brain, normalized CO	Human Fetal Brain				pCMVSPORT 2.0
H0571	Human Fetal Brain, normalized C500HE	Human Fetal Brain				pCMVSPORT 2.0
H0572	Human Fetal Brain, normalized AC5002	Human Fetal Brain				pCMVSPORT 2.0
H0574	Hepatocellular Tumor; re-excision	Hepatocellular Tumor	Liver		disease	Lambda ZAP II
H0575	Human Adult Pulmonary;re-excision	Human Adult Pulmonary	Lung			Uni-ZAP XR
H0576	Resting T-Cell; re-excision	T-Cells	Blood	Cell Line		Lambda ZAP II
H0579	Pericardium	Pericardium	Heart			pSPORT1
H0580	Dendritic cells, pooled	Pooled dendritic cells				pCMVSPORT 3.0
H0581	Human Bone Marrow, treated	Human Bone Marrow	Bone Marrow			pCMVSPORT 3.0
H0583	B Cell lymphoma	B Cell Lymphoma	B Cell		disease	pCMVSPORT 3.0
H0584	Activated T-cells, 24 hrs,re-excision	Activated T-Cells	Blood	Cell Line		Uni-ZAP XR
H0586	Healing groin wound, 6.5 hours post incision	healing groin wound, 6.5 hours post incision - 2/	groin		disease	pCMVSPORT 3.0
H0587	Healing groin wound; 7.5 hours post incision	Groin-2/19/97	groin		disease	pCMVSPORT 3.0
H0589	CD34 positive cells (cord blood),re-ex	CD34 Positive Cells	Cord Blood			ZAP Express
H0590	Human adult small intestine,re-excision	Human Adult Small Intestine	Small Int.			Uni-ZAP XR

H0591	Human T-cell lymphoma;re-excision	T-Cell Lymphoma	T-Cell		disease	Uni-ZAP XR
H0592	Healing groin wound - zero hr post-incision (control)	HGS wound healing project; abdomen			disease	pCMVSPORT 3.0
H0593	Olfactory epithelium;nasalcavity	Olfactory epithelium from roof of left nasal cavity				pCMVSPORT 3.0
H0594	Human Lung Cancer;re-excision	Human Lung Cancer	Lung		disease	Lambda ZAP II
H0595	Stomach cancer (human);re-excision	Stomach Cancer - 5383A (human)			disease	Uni-ZAP XR
H0596	Human Colon Cancer;re-excision	Human Colon Cancer	Colon			Lambda ZAP II
H0597	Human Colon; re-excision	Human Colon				Lambda ZAP II
H0598	Human Stomach;re-excision	Human Stomach	Stomach			Uni-ZAP XR
H0599	Human Adult Heart;re-excision	Human Adult Heart	Heart			Uni-ZAP XR
H0600	Healing Abdomen wound;70&90 min post incision	Abdomen			disease	pCMVSPORT 3.0
H0601	Healing Abdomen Wound;15 days post incision	Abdomen			disease	pCMVSPORT 3.0
H0602	Healing Abdomen Wound;21&29 days post incision	Abdomen			disease	pCMVSPORT 3.0
H0604	Human Pituitary, re-excision	Human Pituitary				pBluescript
H0606	Human Primary Breast Cancer;re-excision	Human Primary Breast Cancer	Breast		disease	Uni-ZAP XR
H0607	H.Leukocytes, normalized cot 50A3	H.Leukocytes				pCMVSPORT 1
H0609	H. Leukocytes, normalized cot > 500A	H.Leukocytes				pCMVSPORT 1
H0610	H. Leukocytes, normalized cot 5A	H.Leukocytes				pCMVSPORT 1
H0611	H. Leukocytes, normalized cot 500 B	H.Leukocytes				pCMVSPORT 1
H0613	H.Leukocytes, normalized cot 5B	H.Leukocytes				pCMVSPORT 1
H0615	Human Ovarian Cancer Reexcision	Ovarian Cancer	Ovary		disease	Uni-ZAP XR
H0616	Human Testes, Reexcision	Human Testes	Testis			Uni-ZAP XR
H0617	Human Primary Breast Cancer Reexcision	Human Primary Breast Cancer	Breast		disease	Uni-ZAP XR
H0618	Human Adult Testes, Large Inserts, Reexcision	Human Adult Testis	Testis			Uni-ZAP XR
H0619	Fetal Heart	Human Fetal Heart	Heart			Uni-ZAP XR
H0620	Human Fetal Kidney; Reexcision	Human Fetal Kidney	Kidney			Uni-ZAP XR
H0622	Human Pancreas Tumor;	Human Pancreas	Pancreas		disease	Uni-ZAP XR

	Reexcision	Tumor				
H0623	Human Umbilical Vein; Reexcision	Human Umbilical Vein Endothelial Cells	Umbilical vein			Uni-ZAP XR
H0624	12 Week Early Stage Human II; Reexcision	Twelve Week Old Early Stage Human	Embryo			Uni-ZAP XR
H0625	Ku 812F Basophils Line	Ku 812F Basophils				pSport1
H0626	Saos2 Cells; Untreated	Saos2 Cell Line; Untreated				pSport1
H0627	Saos2 Cells; Vitamin D3 Treated	Saos2 Cell Line; Vitamin D3 Treated				pSport1
H0628	Human Pre-Differentiated Adipocytes	Human Pre- Differentiated Adipocytes				Uni-ZAP XR
H0629	Human Leukocyte, control #2	Human Normalized leukocyte				pCMVSport 1
H0630	Human Leukocytes,normalized control #4	Human Normalized leukocyte				pCMVSport 1
H0631	Saos2, Dexamethosome Treated	Saos2 Cell Line; Dexamethosome Treated				pSport1
H0632	Hepatocellular Tumor;re- excision	Hepatocellular Tumor	Liver			Lambda ZAP II
H0633	Lung Carcinoma A549 TNFalpha activated	TNFalpha activated A549--Lung Carcinoma			disease	pSport1
H0634	Human Testes Tumor, re- excision	Human Testes Tumor	Testis		disease	Uni-ZAP XR
H0635	Human Activated T-Cells, re-excision	Activated T-Cells	Blood	Cell Line		Uni-ZAP XR
H0637	Dendritic Cells From CD34 Cells	Dendritic cells from CD34 cells				pSport1
H0638	CD40 activated monocyte dendritic cells	CD40 activated monocyte dendritic cells				pSport1
H0641	LPS activated derived dendritic cells	LPS activated monocyte derived dendritic cells				pSport1
H0642	Hep G2 Cells, lambda library	Hep G2 Cells				Other
H0643	Hep G2 Cells, PCR library	Hep G2 Cells				Other
H0644	Human Placenta (re- excision)	Human Placenta	Placenta			Uni-ZAP XR
H0645	Fetal Heart, re-excision	Human Fetal Heart	Heart			Uni-ZAP XR
H0646	Lung, Cancer (400513 A3): Invasive Poorly Differentiated Lung Adenocarcinoma,	Metastatic squamous cell lung carcinoma, poorly di				pSport1
H0647	Lung, Cancer (4005163 B7): Invasive, Poorly Diff. Adenocarcinoma, Metastatic	Invasive poorly differentiated lung adenocarcinoma			disease	pSport1

H0648	Ovary, Cancer: (4004562 B6) Papillary Serous Cystic Neoplasm, Low Malignant Pot	Papillary Cstic neoplasm of low malignant potentia			disease	pSport1
H0649	Lung, Normal: (4005313 B1)	Normal Lung				pSport1
H0650	B-Cells	B-Cells				pCMVSPORT 3.0
H0651	Ovary, Normal: (9805C040R)	Normal Ovary				pSport1
H0652	Lung, Normal: (4005313 B1)	Normal Lung				pSport1
H0653	Stromal Cells	Stromal Cells				pSport1
H0656	B-cells (unstimulated)	B-cells (unstimulated)				pSport1
H0657	B-cells (stimulated)	B-cells (stimulated)				pSport1
H0658	Ovary, Cancer (9809C332): Poorly differentiated adenocarcinoma	9809C332- Poorly differentiate	Ovary & Fallopian Tubes		disease	pSport1
H0659	Ovary, Cancer (15395A1F): Grade II Papillary Carcinoma	Grade II Papillary Carcinoma, Ovary	Ovary		disease	pSport1
H0660	Ovary, Cancer: (15799A1F) Poorly differentiated carcinoma	Poorly differentiated carcinoma, ovary			disease	pSport1
H0661	Breast, Cancer: (4004943 A5)	Breast cancer			disease	pSport1
H0662	Breast, Normal: (4005522B2)	Normal Breast - #4005522(B2)	Breast			pSport1
H0663	Breast, Cancer: (4005522 A2)	Breast Cancer - #4005522(A2)	Breast		disease	pSport1
H0664	Breast, Cancer: (9806C012R)	Breast Cancer	Breast		disease	pSport1
H0665	Stromal cells 3.88	Stromal cells 3.88				pSport1
H0666	Ovary, Cancer: (4004332 A2)	Ovarian Cancer, Sample #4004332A2			disease	pSport1
H0667	Stromal cells(HBM3.18)	Stromal cell(HBM 3.18)				pSport1
H0668	stromal cell clone 2.5	stromal cell clone 2.5				pSport1
H0669	Breast, Cancer: (4005385 A2)	Breast Cancer (4005385A2)	Breast			pSport1
H0670	Ovary, Cancer(4004650 A3): Well-Differentiated Micropapillary Serous Carcinoma	Ovarian Cancer - 4004650A3				pSport1
H0671	Breast, Cancer: (9802C02OE)	Breast Cancer-Sample # 9802C02OE				pSport1
H0672	Ovary, Cancer: (4004576 A8)	Ovarian Cancer(4004576A8)	Ovary			pSport1
H0673	Human Prostate Cancer,	Human Prostate	Prostate			Uni-ZAP XR

	Stage B2; re-excision	Cancer, stage B2				
H0674	Human Prostate Cancer, Stage C; re-excision	Human Prostate Cancer, stage C	Prostate			Uni-ZAP XR
H0675	Colon, Cancer: (9808C064R)	Colon Cancer 9808C064R				pCMVSPORT 3.0
H0676	Colon, Cancer: (9808C064R)-total RNA	Colon Cancer 9808C064R				pCMVSPORT 3.0
H0677	TNFR degenerate oligo	B-Cells				PCR II
H0682	Serous Papillary Adenocarcinoma	serous papillary adenocarcinoma (9606G304SPA3B)				pCMVSPORT 3.0
H0683	Ovarian Serous Papillary Adenocarcinoma	Serous papillary adenocarcinoma, stage 3C (9804G01)				pCMVSPORT 3.0
H0684	Serous Papillary Adenocarcinoma	Ovarian Cancer- 9810G606	Ovaries			pCMVSPORT 3.0
H0685	Adenocarcinoma of Ovary, Human Cell Line, # OVCAR-3	Adenocarcinoma of Ovary, Human Cell Line, # OVCAR-				pCMVSPORT 3.0
H0686	Adenocarcinoma of Ovary, Human Cell Line	Adenocarcinoma of Ovary, Human Cell Line, # SW-626				pCMVSPORT 3.0
H0687	Human normal ovary (#9610G215)	Human normal ovary (#9610G215)	Ovary			pCMVSPORT 3.0
H0688	Human Ovarian Cancer (#9807G017)	Human Ovarian cancer (#9807G017), mRNA from Maura Ru				pCMVSPORT 3.0
H0689	Ovarian Cancer	Ovarian Cancer, #9806G019				pCMVSPORT 3.0
H0690	Ovarian Cancer, # 9702G001	Ovarian Cancer, #9702G001				pCMVSPORT 3.0
H0691	Normal Ovary, #9710G208	normal ovary, #9710G208				pCMVSPORT 3.0
H0693	Normal Prostate #ODQ3958EN	Normal Prostate Tissue # ODQ3958EN				pCMVSPORT 3.0
H0695	mononucleocytes from patient	mononucleocytes from patient at Shady Grove Hospit				pCMVSPORT 3.0
N0006	Human Fetal Brain	Human Fetal Brain				
N0007	Human Hippocampus	Human Hippocampus				
N0009	Human Hippocampus, prescreened	Human Hippocampus				
S0001	Brain frontal cortex	Brain frontal cortex	Brain			Lambda ZAP II
S0002	Monocyte activated	Monocyte-activated	blood	Cell Line		Uni-ZAP XR
S0003	Human Osteoclastoma	Osteoclastoma	bone		disease	Uni-ZAP XR
S0004	Prostate	Prostate BPH	Prostate			Lambda ZAP II
S0005	Heart	Heart-left ventricle	Heart			pCDNA
S0007	Early Stage Human Brain	Human Fetal Brain				Uni-ZAP XR
S0010	Human Amygdala	Amygdala				Uni-ZAP XR
S0011	STROMAL -	Osteoclastoma	bone		disease	Uni-ZAP XR

	OSTEOCLASTOMA					
S0013	Prostate	Prostate	prostate			Uni-ZAP XR
S0016	Kidney Pyramids	Kidney pyramids	Kidney			Uni-ZAP XR
S0022	Human Osteoclastoma Stromal Cells - unamplified	Osteoclastoma Stromal Cells				Uni-ZAP XR
S0026	Stromal cell TF274	stromal cell	Bone marrow	Cell Line		Uni-ZAP XR
S0027	Smooth muscle, serum treated	Smooth muscle	Pulmonary artery	Cell Line		Uni-ZAP XR
S0028	Smooth muscle, control	Smooth muscle	Pulmonary artery	Cell Line		Uni-ZAP XR
S0029	brain stem	Brain stem	brain			Uni-ZAP XR
S0030	Brain pons	Brain Pons	Brain			Uni-ZAP XR
S0031	Spinal cord	Spinal cord	spinal cord			Uni-ZAP XR
S0032	Smooth muscle-ILb induced	Smooth muscle	Pulmonary artery	Cell Line		Uni-ZAP XR
S0036	Human Substantia Nigra	Human Substantia Nigra				Uni-ZAP XR
S0037	Smooth muscle, IL1b induced	Smooth muscle	Pulmonary artery	Cell Line		Uni-ZAP XR
S0038	Human Whole Brain #2 - Oligo dT > 1.5Kb	Human Whole Brain #2				ZAP Express
S0040	Adipocytes	Human Adipocytes from Osteoclastoma				Uni-ZAP XR
S0042	Testes	Human Testes				ZAP Express
S0044	Prostate BPH	prostate BPH	Prostate		disease	Uni-ZAP XR
S0045	Endothelial cells-control	Endothelial cell	endothelial cell-lung	Cell Line		Uni-ZAP XR
S0046	Endothelial-induced	Endothelial cell	endothelial cell-lung	Cell Line		Uni-ZAP XR
S0048	Human Hypothalamus, Alzheimer's	Human Hypothalamus, Alzheimer's			disease	Uni-ZAP XR
S0049	Human Brain, Striatum	Human Brain, Striatum				Uni-ZAP XR
S0050	Human Frontal Cortex, Schizophrenia	Human Frontal Cortex, Schizophrenia			disease	Uni-ZAP XR
S0051	Human Hypothalamus, Schizophrenia	Human Hypothalamus, Schizophrenia			disease	Uni-ZAP XR
S0052	neutrophils control	human neutrophils	blood	Cell Line		Uni-ZAP XR
S0053	Neutrophils IL-1 and LPS induced	human neutrophil induced	blood	Cell Line		Uni-ZAP XR
S0106	STRIATUM DEPRESSION		BRAIN		disease	Uni-ZAP XR
S0112	Hypothalamus		Brain			Uni-ZAP XR
S0114	Anergic T-cell	Anergic T-cell		Cell Line		Uni-ZAP XR
S0116	Bone marrow	Bone marrow	Bone marrow			Uni-ZAP XR
S0122	Osteoclastoma-normalized A	Osteoclastoma	bone		disease	pBluescript
S0126	Osteoblasts	Osteoblasts	Knee	Cell Line		Uni-ZAP XR

S0132	Epithelial-TNF α and INF induced	Airway Epithelial				Uni-ZAP XR
S0134	Apoptotic T-cell	apoptotic cells		Cell Line		Uni-ZAP XR
S0136	PERM TF274	stromal cell	Bone marrow	Cell Line		Lambda ZAP II
S0140	eosinophil-IL5 induced	eosinophil	lung	Cell Line		Uni-ZAP XR
S0142	Macrophage-oxLDL	macrophage-oxidized LDL treated	blood	Cell Line		Uni-ZAP XR
S0144	Macrophage (GM-CSF treated)	Macrophage (GM-CSF treated)				Uni-ZAP XR
S0146	prostate-edited	prostate BPH	Prostate			Uni-ZAP XR
S0148	Normal Prostate	Prostate	prostate			Uni-ZAP XR
S0150	LNCAP prostate cell line	LNCAP Cell Line	Prostate	Cell Line		Uni-ZAP XR
S0152	PC3 Prostate cell line	PC3 prostate cell line				Uni-ZAP XR
S0180	Bone Marrow Stroma, TNF&LPS ind	Bone Marrow Stroma, TNF & LPS induced			disease	Uni-ZAP XR
S0182	Human B Cell 8866	Human B- Cell 8866				Uni-ZAP XR
S0188	Prostate,BPH, Lib 2	Human Prostate BPH			disease	pSport1
S0192	Synovial Fibroblasts (control)	Synovial Fibroblasts				pSport1
S0194	Synovial hypoxia	Synovial Fibroblasts				pSport1
S0196	Synovial IL-1/TNF stimulated	Synovial Fibroblasts				pSport1
S0202	7TM-pbdd	PBLS, 7TM receptor enriched				PCRII
S0206	Smooth Muscle- HASTE normalized	Smooth muscle	Pulmonary artery	Cell Line		pBluescript
S0208	Mesangial cell, frac 1	Mesangial cell				pSport1
S0210	Mesangial cell, frac 2	Mesangial cell				pSport1
S0212	Bone Marrow Stromal Cell, untreated	Bone Marrow Stromal Cell, untreated				pSport1
S0214	Human Osteoclastoma, re-excision	Osteoclastoma	bone		disease	Uni-ZAP XR
S0216	Neutrophils IL-1 and LPS induced	human neutrophil induced	blood	Cell Line		Uni-ZAP XR
S0218	Apoptotic T-cell, re-excision	apoptotic cells		Cell Line		Uni-ZAP XR
S0220	H. hypothalamus, frac A;re-excision	Hypothalamus	Brain			ZAP Express
S0222	H. Frontal cortex,epileptic;re-excision	H. Brain, Frontal Cortex, Epileptic	Brain		disease	Uni-ZAP XR
S0242	Synovial Fibroblasts (II1/TNF), subt	Synovial Fibroblasts				pSport1
S0250	Human Osteoblasts II	Human Osteoblasts	Femur		disease	pCMVSPORT 2.0
S0252	7TM-PIMIX	PBLS, 7TM receptor enriched				PCRII
S0260	Spinal Cord, re-excision	Spinal cord	spinal cord			Uni-ZAP XR
S0268	PRMIX	PRMIX (Human	prostate			PCRII

		Prostate)				
S0270	PTMIX	PTMIX (Human Thymus)	Thymus			PCRII
S0274	PCMIX	PCMIX (Human Cerebellum)	Brain			PCRII
S0276	Synovial hypoxia-RSF subtracted	Synovial fobroblasts (rheumatoid)	Synovial tissue			pSport1
S0278	H Macrophage (GM-CSF treated), re-excision	Macrophage (GM-CSF treated)				Uni-ZAP XR
S0280	Human Adipose Tissue, re-excision	Human Adipose Tissue				Uni-ZAP XR
S0282	Brain Frontal Cortex, re-excision	Brain frontal cortex	Brain			Lambda ZAP II
S0294	Larynx tumor	Larynx tumor	Larynx,vocal cord		disease	pSport1
S0298	Bone marrow stroma,treated	Bone marrow stroma,treatedSB	Bone marrow			pSport1
S0300	Frontal lobe,dementia;re-excision	Frontal Lobe dementia/Alzheimer's	Brain			Uni-ZAP XR
S0306	Larynx normal #10 261-273	Larynx normal				pSport1
S0310	Normal trachea	Normal trachea				pSport1
S0312	Human osteoarthritic;fraction II	Human osteoarthritic cartilage			disease	pSport1
S0314	Human osteoarthritis;fraction I	Human osteoarthritic cartilage			disease	pSport1
S0316	Human Normal Cartilage,Fraction I	Human Normal Cartilage				pSport1
S0318	Human Normal Cartilage Fraction II	Human Normal Cartilage				pSport1
S0322	Siebben Polyposis	Siebben Polyposis				pSport1
S0328	Palate carcinoma	Palate carcinoma	Uvula		disease	pSport1
S0330	Palate normal	Palate normal	Uvula			pSport1
S0332	Pharynx carcinoma	Pharynx carcinoma	Hypopharynx			pSport1
S0334	Human Normal Cartilage Fraction III	Human Normal Cartilage				pSport1
S0336	Human Normal Cartilage Fraction IV	Human Normal Cartilage				pSport1
S0338	Human Osteoarthritic Cartilage Fraction III	Human osteoarthritic cartilage			disease	pSport1
S0340	Human Osteoarthritic Cartilage Fraction IV	Human osteoarthritic cartilage			disease	pSport1
S0342	Adipocytes;re-excision	Human Adipocytes from Osteoclastoma				Uni-ZAP XR
S0344	Macrophage-oxLDL; re-excision	macrophage-oxidized LDL treated	blood	Cell Line		Uni-ZAP XR
S0346	Human Amygdala;re-	Amygdala				Uni-ZAP XR

	excision					
S0348	Cheek Carcinoma	Cheek Carcinoma			disease	pSport1
S0350	Pharynx Carcinoma	Pharynx carcinoma	Hypopharynx		disease	pSport1
S0352	Larynx Carcinoma	Larynx carcinoma			disease	pSport1
S0354	Colon Normal II	Colon Normal	Colon			pSport1
S0356	Colon Carcinoma	Colon Carcinoma	Colon		disease	pSport1
S0358	Colon Normal III	Colon Normal	Colon			pSport1
S0360	Colon Tumor II	Colon Tumor	Colon		disease	pSport1
S0362	Human Gastrocnemius	Gastrocnemius muscle				pSport1
S0364	Human Quadriceps	Quadriceps muscle				pSport1
S0366	Human Soleus	Soleus Muscle				pSport1
S0368	Human Pancreatic Langerhans	Islets of Langerhans				pSport1
S0370	Larynx carcinoma II	Larynx carcinoma			disease	pSport1
S0374	Normal colon	Normal colon				pSport1
S0376	Colon Tumor	Colon Tumor			disease	pSport1
S0378	Pancreas normal PCA4 No	Pancreas Normal PCA4 No				pSport1
S0380	Pancreas Tumor PCA4 Tu	Pancreas Tumor PCA4 Tu			disease	pSport1
S0384	Tongue carcinoma	Tongue carcinoma			disease	pSport1
S0386	Human Whole Brain, re-excision	Whole brain	Brain			ZAP Express
S0388	Human Hypothalamus, schizophrenia, re-excision	Human Hypothalamus, Schizophrenia			disease	Uni-ZAP XR
S0390	Smooth muscle, control; re-excision	Smooth muscle	Pulmonary artery	Cell Line		Uni-ZAP XR
S0392	Salivary Gland	Salivary gland; normal				pSport1
S0400	Brain; normal	Brain; normal				pSport1
S0404	Rectum normal	Rectum, normal				pSport1
S0406	Rectum tumour	Rectum tumour				pSport1
S0408	Colon, normal	Colon, normal				pSport1
S0412	Temporal cortex- Alzheimer; subtracted	Temporal cortex, alzheimer			disease	Other
S0414	Hippocampus, Alzheimer Subtracted	Hippocampus, Alzheimer Subtracted				Other
S0418	CHME Cell Line; treated 5 hrs	CHME Cell Line; treated				pCMV Sport 3.0
S0420	CHME Cell Line, untreated	CHME Cell line, untreated				pSport1
S0422	Mo7e Cell Line GM-CSF treated (1ng/ml)	Mo7e Cell Line GM-CSF treated (1ng/ml)				pCMV Sport 3.0
S0424	TF-1 Cell Line GM-CSF Treated	TF-1 Cell Line GM-CSF Treated				pSport1
S0426	Monocyte activated; re-excision	Monocyte-activated	blood	Cell Line		Uni-ZAP XR
S0428	Neutrophils control; re-	human neutrophils	blood	Cell Line		Uni-ZAP XR

	excision					
S0430	Aryepiglottis Normal	Aryepiglottis Normal				pSport1
S0432	Sinus piniformis Tumour	Sinus piniformis Tumour				pSport1
S0434	Stomach Normal	Stomach Normal			disease	pSport1
S0436	Stomach Tumour	Stomach Tumour			disease	pSport1
S0440	Liver Tumour Met 5 Tu	Liver Tumour				pSport1
S0442	Colon Normal	Colon Normal				pSport1
S0444	Colon Tumor	Colon Tumour			disease	pSport1
S0446	Tongue Tumour	Tongue Tumour				pSport1
S0448	Larynx Normal	Larynx Normal				pSport1
S0450	Larynx Tumour	Larynx Tumour				pSport1
S0452	Thymus	Thymus				pSport1
S0454	Placenta	Placenta	Placenta			pSport1
S0456	Tongue Normal	Tongue Normal				pSport1
S0458	Thyroid Normal (SDCA2 No)	Thyroid normal				pSport1
S0462	Thyroid Thyroiditis	Thyroid Thyroiditis				pSport1
S0464	Larynx Normal	Larynx Normal				pSport1
S0466	Larynx Tumor	Larynx Tumor			disease	pSport1
S0468	Ea.hy.926 cell line	Ea.hy.926 cell line				pSport1
S0470	Adenocarcinoma	PYFD			disease	pSport1
S0472	Lung Mesothelium	PYBT				pSport1
S0474	Human blood platelets	Platelets	Blood platelets			Other
S0665	Human Amygdala; re-excision	Amygdala				Uni-ZAP XR
S3012	Smooth Muscle Serum Treated, Norm	Smooth muscle	Pulmonary artery	Cell Line		pBluescript
S3014	Smooth muscle, serum induced,re-exc	Smooth muscle	Pulmonary artery	Cell Line		pBluescript
S6014	H. hypothalamus, frac A	Hypothalamus	Brain			ZAP Express
S6016	H. Frontal Cortex, Epileptic	H. Brain, Frontal Cortex, Epileptic	Brain		disease	Uni-ZAP XR
S6022	H. Adipose Tissue	Human Adipose Tissue				Uni-ZAP XR
S6024	Alzheimers, spongy change	Alzheimer's/Spongy change	Brain		disease	Uni-ZAP XR
S6026	Frontal Lobe, Dementia	Frontal Lobe dementia/Alzheimer's	Brain			Uni-ZAP XR
S6028	Human Manic Depression Tissue	Human Manic depression tissue	Brain		disease	Uni-ZAP XR
T0002	Activated T-cells	Activated T-Cell, PBL fraction	Blood	Cell Line		pBluescript SK-
T0003	Human Fetal Lung	Human Fetal Lung				pBluescript SK-
T0004	Human White Fat	Human White Fat				pBluescript SK-
T0006	Human Pineal Gland	Human Pinneal Gland				pBluescript SK-
T0008	Colorectal Tumor	Colorectal Tumor			disease	pBluescript SK-
T0010	Human Infant Brain	Human Infant Brain				Other

T0023	Human Pancreatic Carcinoma	Human Pancreatic Carcinoma			disease	pBluescript SK-
T0039	HSA 172 Cells	Human HSA172 cell line				pBluescript SK-
T0040	HSC172 cells	SA172 Cells				pBluescript SK-
T0041	Jurkat T-cell G1 phase	Jurkat T-cell				pBluescript SK-
T0042	Jurkat T-Cell, S phase	Jurkat T-Cell Line				pBluescript SK-
T0048	Human Aortic Endothelium	Human Aortic Endothilium				pBluescript SK-
T0049	Aorta endothelial cells + TNF-a	Aorta endothelial cells				pBluescript SK-
T0060	Human White Adipose	Human White Fat				pBluescript SK-
T0067	Human Thyroid	Human Thyroid				pBluescript SK-
T0068	Normal Ovary, Premenopausal	Normal Ovary, Premenopausal				pBluescript SK-
T0069	Human Uterus, normal	Human Uterus, normal				pBluescript SK-
T0071	Human Bone Marrow	Human Bone Marrow				pBluescript SK-
T0074	Human Adult Retina	Human Adult Retina				pBluescript SK-
T0079	Human Kidney, normal Adult	Human Kidney, normal Adult				pBluescript SK-
T0082	Human Adult Retina	Human Adult Retina				pBluescript SK-
T0103	Human colon carcinoma (HCC) cell line					pBluescript SK-
T0104	HCC cell line metastasis to liver					pBluescript SK-
T0109	Human (HCC) cell line liver (mouse) metastasis, remake					pBluescript SK-
T0110	Human colon carcinoma (HCC) cell line, remake					pBluescript SK-
T0114	Human (Caco-2) cell line, adenocarcinoma, colon, remake					pBluescript SK-
T0115	Human Colon Carcinoma (HCC) cell line					pBluescript SK-
L0002	Atrium cDNA library Human heart					
L0005	Clontech human aorta polyA+ mRNA (#6572)					
L0010	GeneTrack, 4p16.3 JM Rommens					
L0021	Human adult (K.Okubo)					
L0022	Human adult lung 3" directed MboI cDNA					
L0034	Human chromosome 14					
L0040	Human colon mucosa					
L0055	Human promyelocyte					
L0060	Human thymus NSTH II					
L0103	DKFZphamy1	amygdala				
L0105	Human aorta polyA+	aorta				

	(TFujiwara)					
L0119	human glioblastoma library	brain				
L0142	Human placenta cDNA (TFujiwara)	placenta				
L0143	Human placenta polyA+ (TFujiwara)	placenta				
L0157	Human fetal brain (TFujiwara)		brain			
L0163	Human heart cDNA (YNakamura)		heart			
L0183	Human HeLa cells (M.Lovett)			HeLa		
L0193	Human osteosarcoma EGracia	osteosarcoma		OsA-CL		
L0194	Human pancreatic cancer cell line Patu 8988t	pancreatic cancer		Patu 8988t		
L0351	Infant brain, Bento Soares					BA, M13-derived
L0352	Normalized infant brain, Bento Soares					BA, M13-derived
L0356	S, Human foetal Adrenals tissue					Bluescript
L0361	Stratagene ovary (#937217)		ovary			Bluescript SK
L0362	Stratagene ovarian cancer (#937219)					Bluescript SK-
L0363	NCI_CGAP_GC2	germ cell tumor				Bluescript SK-
L0364	NCI_CGAP_GC5	germ cell tumor				Bluescript SK-
L0366	Stratagene schizo brain S11	schizophrenic brain S-11 frontal lobe				Bluescript SK-
L0367	NCI_CGAP_Sch1	Schwannoma tumor				Bluescript SK-
L0368	NCI_CGAP_SS1	synovial sarcoma				Bluescript SK-
L0369	NCI_CGAP_AA1	adrenal adenoma	adrenal gland			Bluescript SK-
L0370	Johnston frontal cortex	pooled frontal lobe	brain			Bluescript SK-
L0371	NCI_CGAP_Br3	breast tumor	breast			Bluescript SK-
L0372	NCI_CGAP_Co12	colon tumor	colon			Bluescript SK-
L0373	NCI_CGAP_Co11	tumor	colon			Bluescript SK-
L0374	NCI_CGAP_Co2	tumor	colon			Bluescript SK-
L0375	NCI_CGAP_Kid6	kidney tumor	kidney			Bluescript SK-
L0376	NCI_CGAP_Lar1	larynx	larynx			Bluescript SK-
L0378	NCI_CGAP_Lu1	lung tumor	lung			Bluescript SK-
L0381	NCI_CGAP_HN4	squamous cell carcinoma	pharynx			Bluescript SK-
L0382	NCI_CGAP_Pr25	epithelium (cell line)	prostate			Bluescript SK-
L0383	NCI_CGAP_Pr24	invasive tumor (cell line)	prostate			Bluescript SK-
L0384	NCI_CGAP_Pr23	prostate tumor	prostate			Bluescript SK-
L0385	NCI_CGAP_Gas1	gastric tumor	stomach			Bluescript SK-
L0387	NCI_CGAP_GCB0	germinal center B-cells	tonsil			Bluescript SK-
L0388	NCI_CGAP_HN6	normal gingiva (cell				Bluescript SK-

		line from immortalized kerati				
L0389	NCI_CGAP_HN5	normal gingiva (cell line from primary keratinocyt				Bluescript SK-
L0394	H, Human adult Brain Cortex tissue					gt11
L0411	1-NIB					Lafmid BA
L0435	Infant brain, LLNL array of Dr. M. Soares 1NIB					lafmid BA
L0438	normalized infant brain cDNA	total brain	brain			lafmid BA
L0439	Soares infant brain 1NIB		whole brain			Lafmid BA
L0441	2HB3MK					Lafmid BK
L0448	3HFLSK20					Lafmid K
L0455	Human retina cDNA randomly primed sublibrary	retina	eye			lambda gt10
L0456	Human retina cDNA Tsp509I-cleaved sublibrary	retina	eye			lambda gt10
L0465	TEST1, Human adult Testis tissue					lambda nm1149
L0471	Human fetal heart, Lambda ZAP Express					Lambda ZAP Express
L0475	KG1-a Lambda Zap Express cDNA library			KG1-a		Lambda Zap Express (Stratagene)
L0477	HPLA CCLee	placenta				Lambda ZAP II
L0480	Stratagene cat#937212 (1992)					Lambda ZAP, pBluescript SK(-)
L0481	CD34+DIRECTIONAL					Lambda ZAPII
L0483	Human pancreatic islet					Lambda ZAPII
L0485	STRATAGENE Human skeletal muscle cDNA library, cat. #936215.	skeletal muscle	leg muscle			Lambda ZAPII
L0493	NCI_CGAP_Ov26	papillary serous carcinoma	ovary			pAMP1
L0497	NCI_CGAP_HSC4	CD34+, CD38- from normal bone marrow donor	bone marrow			pAMP1
L0498	NCI_CGAP_HSC3	CD34+, T negative, patient with chronic myelogenou	bone marrow			pAMP1
L0500	NCI_CGAP_Brn20	oligodendroglioma	brain			pAMP1
L0502	NCI_CGAP_Br15	adenocarcinoma	breast			pAMP1
L0508	NCI_CGAP_Lu25	bronchioalveolar carcinoma	lung			pAMP1
L0509	NCI_CGAP_Lu26	invasive adenocarcinoma	lung			pAMP1
L0514	NCI_CGAP_Ov31	papillary serous carcinoma	ovary			pAMP1

L0515	NCI_CGAP_Ov32	papillary serous carcinoma	ovary			pAMP1
L0517	NCI_CGAP_Pr1					pAMP10
L0518	NCI_CGAP_Pr2					pAMP10
L0519	NCI_CGAP_Pr3					pAMP10
L0520	NCI_CGAP_Alv1	alveolar rhabdomyosarcoma				pAMP10
L0521	NCI_CGAP_Ew1	Ewing's sarcoma				pAMP10
L0523	NCI_CGAP_Lip2	liposarcoma				pAMP10
L0525	NCI_CGAP_Li2	liver				pAMP10
L0526	NCI_CGAP_Pr12	metastatic prostate bone lesion				pAMP10
L0527	NCI_CGAP_Ov2	ovary				pAMP10
L0528	NCI_CGAP_Pr5	prostate				pAMP10
L0529	NCI_CGAP_Pr6	prostate				pAMP10
L0530	NCI_CGAP_Pr8	prostate				pAMP10
L0532	NCI_CGAP_Thy1	thyroid				pAMP10
L0533	NCI_CGAP_HSC1	stem cells	bone marrow			pAMP10
L0536	NCI_CGAP_Br4	normal ductal tissue	breast			pAMP10
L0540	NCI_CGAP_Pr10	invasive prostate tumor	prostate			pAMP10
L0541	NCI_CGAP_Pr7	low-grade prostatic neoplasia	prostate			pAMP10
L0542	NCI_CGAP_Pr11	normal prostatic epithelial cells	prostate			pAMP10
L0543	NCI_CGAP_Pr9	normal prostatic epithelial cells	prostate			pAMP10
L0544	NCI_CGAP_Pr4	prostatic intraepithelial neoplasia - high grade	prostate			pAMP10
L0545	NCI_CGAP_Pr4.1	prostatic intraepithelial neoplasia - high grade	prostate			pAMP10
L0546	NCI_CGAP_Pr18	stroma	prostate			pAMP10
L0547	NCI_CGAP_Pr16	tumor	prostate			pAMP10
L0549	NCI_CGAP_HN10	carcinoma in situ from retromolar trigone				pAMP10
L0557	NCI_CGAP_Lu21	small cell carcinoma	lung			pAMP10
L0558	NCI_CGAP_Ov40	endometrioid ovarian metastasis	ovary			pAMP10
L0561	NCI_CGAP_HN11	normal squamous epithelium	tongue			pAMP10
L0563	Human Bone Marrow Stromal Fibroblast	bone marrow				pBluescript
L0564	Jia bone marrow stroma	bone marrow stroma				pBluescript
L0565	Normal Human Trabecular Bone Cells	Bone	Hip			pBluescript
L0579	Human fetal brain QBogin2	cerebrum and cerebellum				pBluescript SK

L0581	Stratagene liver (#937224)		liver			pBluescript SK
L0584	Stratagene cDNA library Human heart, cat#936208					pBluescript SK(+)
L0586	HTCDL1					pBluescript SK(-)
L0587	Stratagene colon HT29 (#937221)					pBluescript SK-
L0588	Stratagene endothelial cell 937223					pBluescript SK-
L0589	Stratagene fetal retina 937202					pBluescript SK-
L0590	Stratagene fibroblast (#937212)					pBluescript SK-
L0591	Stratagene HeLa cell s3 937216					pBluescript SK-
L0592	Stratagene hNT neuron (#937233)					pBluescript SK-
L0593	Stratagene neuroepithelium (#937231)					pBluescript SK-
L0594	Stratagene neuroepithelium NT2RAMI 937234					pBluescript SK-
L0595	Stratagene NT2 neuronal precursor 937230	neuroepithelial cells	brain			pBluescript SK-
L0596	Stratagene colon (#937204)		colon			pBluescript SK-
L0597	Stratagene corneal stroma (#937222)		cornea			pBluescript SK-
L0598	Morton Fetal Cochlea	cochlea	ear			pBluescript SK-
L0599	Stratagene lung (#937210)		lung			pBluescript SK-
L0600	Weizmann Olfactory Epithelium	olfactory epithelium	nose			pBluescript SK-
L0601	Stratagene pancreas (#937208)		pancreas			pBluescript SK-
L0602	Pancreatic Islet	pancreatic islet	pancreas			pBluescript SK-
L0603	Stratagene placenta (#937225)		placenta			pBluescript SK-
L0604	Stratagene muscle 937209	muscle	skeletal muscle			pBluescript SK-
L0605	Stratagene fetal spleen (#937205)	fetal spleen	spleen			pBluescript SK-
L0606	NCL_CGAP_Lym5	follicular lymphoma	lymph node			pBluescript SK-
L0607	NCL_CGAP_Lym6	mantle cell lymphoma	lymph node			pBluescript SK-
L0608	Stratagene lung carcinoma 937218	lung carcinoma	lung	NCI-H69		pBluescript SK-
L0611	Schiller meningioma	meningioma	brain			pBluescript SK- (Stratagene)
L0615	22 week old human fetal liver cDNA library					pBluescriptII SK(-)
L0617	Chromosome 22 exon					pBluescriptIIKS +

L0618	Chromosome 9 exon					pBluescriptIIKS +
L0619	Chromosome 9 exon II					pBluescriptIIKS +
L0622	HM1					pcDNAII (Invitrogen)
L0623	HM3	pectoral muscle (after mastectomy)				pcDNAII (Invitrogen)
L0625	NCI_CGAP_AR1	bulk alveolar tumor				pCMV-SPORT2
L0626	NCI_CGAP_GC1	bulk germ cell seminoma				pCMV-SPORT2
L0628	NCI_CGAP_Ov1	ovary bulk tumor	ovary			pCMV-SPORT2
L0629	NCI_CGAP_Mel3	metastatic melanoma to bowel	bowel (skin primary)			pCMV-SPORT4
L0630	NCI_CGAP_CNS1	substantia nigra	brain			pCMV-SPORT4
L0631	NCI_CGAP_Br7		breast			pCMV-SPORT4
L0632	NCI_CGAP_Li5	hepatic adenoma	liver			pCMV-SPORT4
L0634	NCI_CGAP_Ov8	serous adenocarcinoma	ovary			pCMV-SPORT4
L0635	NCI_CGAP_PNS1	dorsal root ganglion	peripheral nervous system			pCMV-SPORT4
L0636	NCI_CGAP_Pit1	four pooled pituitary adenomas	brain			pCMV-SPORT6
L0637	NCI_CGAP_Brn53	three pooled meningiomas	brain			pCMV-SPORT6
L0638	NCI_CGAP_Brn35	tumor, 5 pooled (see description)	brain			pCMV-SPORT6
L0639	NCI_CGAP_Brn52	tumor, 5 pooled (see description)	brain			pCMV-SPORT6
L0640	NCI_CGAP_Br18	four pooled high-grade tumors, including two prima	breast			pCMV-SPORT6
L0641	NCI_CGAP_Co17	juvenile granulosa tumor	colon			pCMV-SPORT6
L0642	NCI_CGAP_Co18	moderately differentiated adenocarcinoma	colon			pCMV-SPORT6
L0643	NCI_CGAP_Co19	moderately differentiated adenocarcinoma	colon			pCMV-SPORT6
L0644	NCI_CGAP_Co20	moderately differentiated adenocarcinoma	colon			pCMV-SPORT6
L0645	NCI_CGAP_Co21	moderately differentiated adenocarcinoma	colon			pCMV-SPORT6
L0646	NCI_CGAP_Co14	moderately-differentiated adenocarcinoma	colon			pCMV-SPORT6
L0647	NCI_CGAP_Sar4	five pooled sarcomas, including myxoid liposarcoma	connective tissue			pCMV-SPORT6

L0648	NCI_CGAP_Eso2	squamous cell carcinoma	esophagus			pCMV-SPORT6
L0649	NCI_CGAP_GU1	2 pooled high-grade transitional cell tumors	genitourinary tract			pCMV-SPORT6
L0650	NCI_CGAP_Kid13	2 pooled Wilms" tumors, one primary and one metast	kidney			pCMV-SPORT6
L0651	NCI_CGAP_Kid8	renal cell tumor	kidney			pCMV-SPORT6
L0652	NCI_CGAP_Lu27	four pooled poorly-differentiated adenocarcinomas	lung			pCMV-SPORT6
L0653	NCI_CGAP_Lu28	two pooled squamous cell carcinomas	lung			pCMV-SPORT6
L0654	NCI_CGAP_Lu31		lung, cell line			pCMV-SPORT6
L0655	NCI_CGAP_Lym12	lymphoma, follicular mixed small and large cell	lymph node			pCMV-SPORT6
L0656	NCI_CGAP_Ov38	normal epithelium	ovary			pCMV-SPORT6
L0657	NCI_CGAP_Ov23	tumor, 5 pooled (see description)	ovary			pCMV-SPORT6
L0658	NCI_CGAP_Ov35	tumor, 5 pooled (see description)	ovary			pCMV-SPORT6
L0659	NCI_CGAP_Pan1	adenocarcinoma	pancreas			pCMV-SPORT6
L0661	NCI_CGAP_Mel15	malignant melanoma, metastatic to lymph node	skin			pCMV-SPORT6
L0662	NCI_CGAP_Gas4	poorly differentiated adenocarcinoma with signet r	stomach			pCMV-SPORT6
L0663	NCI_CGAP_Ut2	moderately-differentiated endometrial adenocarcino	uterus			pCMV-SPORT6
L0664	NCI_CGAP_Ut3	poorly-differentiated endometrial adenocarcinoma,	uterus			pCMV-SPORT6
L0665	NCI_CGAP_Ut4	serous papillary carcinoma, high grade, 2 pooled t	uterus			pCMV-SPORT6
L0666	NCI_CGAP_Ut1	well-differentiated endometrial adenocarcinoma, 7	uterus			pCMV-SPORT6
L0667	NCI_CGAP_CML1	myeloid cells, 18 pooled CML cases, BCR/ABL rearra	whole blood			pCMV-SPORT6
L0684	Stanley Frontal SB pool 1	frontal lobe (see description)	brain			pCR2.1-TOPO (Invitrogen)
L0686	Stanley Frontal SN pool 2	frontal lobe (see description)	brain			pCR2.1-TOPO (Invitrogen)
L0697	Testis 1					PGEM 5zf(+)

L0698	Testis 2					PGEM 5zf(+)
L0717	Gessler Wilms tumor					pSPORT1
L0731	Soares_pregnant_uterus_NbHPU		uterus			pT7T3-Pac
L0738	Human colorectal cancer					pT7T3D
L0740	Soares melanocyte 2NbHM	melanocyte				pT7T3D (Pharmacia) with a modified polylinker
L0741	Soares adult brain N2b4HB55Y		brain			pT7T3D (Pharmacia) with a modified polylinker
L0742	Soares adult brain N2b5HB55Y		brain			pT7T3D (Pharmacia) with a modified polylinker
L0743	Soares breast 2NbHBst		breast			pT7T3D (Pharmacia) with a modified polylinker
L0744	Soares breast 3NbHBst		breast			pT7T3D (Pharmacia) with a modified polylinker
L0745	Soares retina N2b4HR	retina	eye			pT7T3D (Pharmacia) with a modified polylinker
L0746	Soares retina N2b5HR	retina	eye			pT7T3D (Pharmacia) with a modified polylinker
L0747	Soares_fetal_heart_NbHH 19W		heart			pT7T3D (Pharmacia) with a modified polylinker
L0748	Soares fetal liver spleen 1NFLS		Liver and Spleen			pT7T3D (Pharmacia) with a modified polylinker
L0749	Soares_fetal_liver_spleen_1NFLS_S1		Liver and Spleen			pT7T3D (Pharmacia) with a modified polylinker
L0750	Soares_fetal_lung_NbHL1 9W		lung			pT7T3D (Pharmacia) with a modified polylinker
L0751	Soares ovary tumor NbHOT	ovarian tumor	ovary			pT7T3D (Pharmacia) with a modified polylinker

L0752	Soares_parathyroid_tumor_NbHPA	parathyroid tumor	parathyroid gland			pT7T3D (Pharmacia) with a modified polylinker
L0753	Soares_pineal_gland_N3H PG		pineal gland			pT7T3D (Pharmacia) with a modified polylinker
L0754	Soares_placenta Nb2HP		placenta			pT7T3D (Pharmacia) with a modified polylinker
L0755	Soares_placenta_8to9weeks_2NbHP8to9W		placenta			pT7T3D (Pharmacia) with a modified polylinker
L0756	Soares_multiple_sclerosis_2NbHMSP	multiple sclerosis lesions				pT7T3D (Pharmacia) with a modified polylinker V_TYPE
L0757	Soares_senescent_fibroblasts_NbHSF	senescent fibroblast				pT7T3D (Pharmacia) with a modified polylinker V_TYPE
L0758	Soares_testis_NHT					pT7T3D-Pac (Pharmacia) with a modified polylinker
L0759	Soares_total_fetus_Nb2HF8_9w					pT7T3D-Pac (Pharmacia) with a modified polylinker
L0760	Barstead aorta HPLRB3	aorta				pT7T3D-Pac (Pharmacia) with a modified polylinker
L0761	NCI_CGAP_CLL1	B-cell, chronic lymphocytic leukemia				pT7T3D-Pac (Pharmacia) with a modified polylinker
L0762	NCI_CGAP_Br1.1	breast				pT7T3D-Pac (Pharmacia) with a modified polylinker
L0763	NCI_CGAP_Br2	breast				pT7T3D-Pac (Pharmacia) with a modified polylinker
L0764	NCI_CGAP_Co3	colon				pT7T3D-Pac (Pharmacia) with a modified polylinker

L0765	NCI_CGAP_Co4	colon				pT7T3D-Pac (Pharmacia) with a modified polylinker
L0766	NCI_CGAP_GCB1	germinal center B cell				pT7T3D-Pac (Pharmacia) with a modified polylinker
L0767	NCI_CGAP_GC3	pooled germ cell tumors				pT7T3D-Pac (Pharmacia) with a modified polylinker
L0768	NCI_CGAP_GC4	pooled germ cell tumors				pT7T3D-Pac (Pharmacia) with a modified polylinker
L0769	NCI_CGAP_Brn25	anaplastic oligodendroglioma	brain			pT7T3D-Pac (Pharmacia) with a modified polylinker
L0770	NCI_CGAP_Brn23	glioblastoma (pooled)	brain			pT7T3D-Pac (Pharmacia) with a modified polylinker
L0771	NCI_CGAP_Co8	adenocarcinoma	colon			pT7T3D-Pac (Pharmacia) with a modified polylinker
L0772	NCI_CGAP_Co10	colon tumor RER+	colon			pT7T3D-Pac (Pharmacia) with a modified polylinker
L0773	NCI_CGAP_Co9	colon tumor RER+	colon			pT7T3D-Pac (Pharmacia) with a modified polylinker
L0774	NCI_CGAP_Kid3		kidney			pT7T3D-Pac (Pharmacia) with a modified polylinker
L0775	NCI_CGAP_Kid5	2 pooled tumors (clear cell type)	kidney			pT7T3D-Pac (Pharmacia) with a modified polylinker
L0776	NCI_CGAP_Lu5	carcinoid	lung			pT7T3D-Pac (Pharmacia) with a modified polylinker
L0777	Soares_NhHMPu_S1	Pooled human melanocyte, fetal heart, and pregnant	mixed (see below)			pT7T3D-Pac (Pharmacia) with a modified polylinker
L0779	Soares_NFL_T_GBC_S1		pooled			pT7T3D-Pac (Pharmacia)

						with a modified polylinker
L0780	Soares_NSF_F8_9W_OT_PA_P_S1		pooled			pT7T3D-Pac (Pharmacia) with a modified polylinker
L0782	NCI_CGAP_Pr21	normal prostate	prostate			pT7T3D-Pac (Pharmacia) with a modified polylinker
L0783	NCI_CGAP_Pr22	normal prostate	prostate			pT7T3D-Pac (Pharmacia) with a modified polylinker
L0784	NCI_CGAP_Lei2	leiomyosarcoma	soft tissue			pT7T3D-Pac (Pharmacia) with a modified polylinker
L0785	Barstead spleen HPLRB2		spleen			pT7T3D-Pac (Pharmacia) with a modified polylinker
L0786	Soares_NbHFB		whole brain			pT7T3D-Pac (Pharmacia) with a modified polylinker
L0787	NCI_CGAP_Sub1					pT7T3D-Pac (Pharmacia) with a modified polylinker
L0788	NCI_CGAP_Sub2					pT7T3D-Pac (Pharmacia) with a modified polylinker
L0789	NCI_CGAP_Sub3					pT7T3D-Pac (Pharmacia) with a modified polylinker
L0790	NCI_CGAP_Sub4					pT7T3D-Pac (Pharmacia) with a modified polylinker
L0791	NCI_CGAP_Sub5					pT7T3D-Pac (Pharmacia) with a modified polylinker
L0792	NCI_CGAP_Sub6					pT7T3D-Pac (Pharmacia) with a modified polylinker
L0794	NCI_CGAP_GC6	pooled germ cell tumors				pT7T3D-Pac (Pharmacia) with a modified polylinker

L0796	NCI_CGAP_Brn50	medulloblastoma	brain			pT7T3D-Pac (Pharmacia) with a modified polylinker
L0800	NCI_CGAP_Co16	colon tumor, RER+	colon			pT7T3D-Pac (Pharmacia) with a modified polylinker
L0803	NCI_CGAP_Kid11		kidney			pT7T3D-Pac (Pharmacia) with a modified polylinker
L0804	NCI_CGAP_Kid12	2 pooled tumors (clear cell type)	kidney			pT7T3D-Pac (Pharmacia) with a modified polylinker
L0805	NCI_CGAP_Lu24	carcinoid	lung			pT7T3D-Pac (Pharmacia) with a modified polylinker
L0806	NCI_CGAP_Lu19	squamous cell carcinoma, poorly differentiated (4	lung			pT7T3D-Pac (Pharmacia) with a modified polylinker
L0807	NCI_CGAP_Ov18	fibrotheoma	ovary			pT7T3D-Pac (Pharmacia) with a modified polylinker
L0808	Barstead prostate BPH HPLRB4 1		prostate			pT7T3D-Pac (Pharmacia) with a modified polylinker
L0809	NCI_CGAP_Pr28		prostate			pT7T3D-Pac (Pharmacia) with a modified polylinker
L2250	Human cerebral cortex	cerebral cortex				
L2251	Human fetal lung	Fetal lung				

TABLE 5

OMIM Reference	Description
103050	Autism, succinylpurinemic
103050	Adenylosuccinase deficiency
104770	Amyloidosis, secondary, susceptibility to
106180	Myocardial infarction, susceptibility to
107670	Apolipoprotein A-II deficiency
108725	Atherosclerosis, susceptibility to
109690	Asthma, nocturnal, susceptibility to
109690	Obesity, susceptibility to
110700	Vivax malaria, susceptibility to
114290	Campomelic dysplasia with autosomal sex reversal
115660	Cataract, cerulean, type 1
116860	Cavernous angiomatous malformations
120700	C3 deficiency
121050	Contractural arachnodactyly, congenital
123101	Craniosynostosis, type 2
124030	Parkinsonism, susceptibility to
124030	Debrisoquine sensitivity
126150	Diphtheria, susceptibility to
126337	Myxoid liposarcoma
126650	Chloride diarrhea, congenital, Finnish type, 214700
126650	Colon cancer
129900	EEC syndrome-1
133170	Erythremia
133171	[Erythrocytosis, familial], 133100
135940	Ichthyosis vulgaris, 146700
136836	Fucosyltransferase-6 deficiency
138033	Diabetes mellitus, type II
138700	[Apolipoprotein H deficiency]
138981	Pulmonary alveolar proteinosis, 265120
139190	Gigantism due to GHRF hypersecretion
139190	Isolated growth hormone deficiency due to defect in GHRF
139250	Isolated growth hormone deficiency, Illig type with absent GH and Kowarski type with bioinactive GH
141750	Alpha-thalassemia/mental retardation syndrome, type 1
141800	Methemoglobinemias, alpha-
141800	Thalassemias, alpha-
141800	Erythremias, alpha-
141800	Heinz body anemias, alpha-
141850	Thalassemia, alpha-
141850	Erythrocytosis
141850	Heinz body anemia
141850	Hemoglobin H disease
141850	Hypochromic microcytic anemia

145001	Hyperparathyroidism-jaw tumor syndrome
145981	Hypocalciuric hypercalcemia, type II
146790	Lupus nephritis, susceptibility to
147141	Leukemia, acute lymphoblastic
148500	Tylosis with esophageal cancer
150200	[Placental lactogen deficiency]
152445	Vohwinkel syndrome, 124500
152445	Erythrokeratoderma, progressive symmetric, 602036
154275	Malignant hyperthermia susceptibility 2
154276	Malignant hyperthermia susceptibility 3
156850	Cataract, congenital, with microphthalmia
159000	Muscular dystrophy, limb-girdle, type 1A
159001	Muscular dystrophy, limb-girdle, type 1B
162100	Neuralgic amyotrophy with predilection for brachial plexus
164953	Liposarcoma
170500	Myotonia congenita, atypical acetazolamide-responsive
170500	Paramyotonia congenita, 168300
170500	Hyperkalemic periodic paralysis
173360	Thrombophilia due to excessive plasminogen activator inhibitor
173360	Hemorrhagic diathesis due to PAI1 deficiency
174000	Medullary cystic kidney disease, AD
174900	Polyposis, juvenile intestinal
176960	Pituitary tumor, invasive
179095	Male infertility
179755	Renal cell carcinoma, papillary, 1
180071	Retinitis pigmentosa, autosomal recessive
180860	Russell-Silver syndrome
182380	Glucose/galactose malabsorption
182452	Lung cancer, small cell
182860	Pyropoikilocytosis
182860	Spherocytosis, recessive
182860	Elliptocytosis-2
186580	Arthrocutaneous uveal granulomatosis
188070	Bleeding disorder due to defective thromboxane A2 receptor
188826	Sorsby fundus dystrophy, 136900
190040	Dermatofibrosarcoma protuberans
190040	Giant-cell fibroblastoma
190040	Meningioma, SIS-related
191092	Tuberous sclerosis-2
191315	Insensitivity to pain, congenital, with anhidrosis, 256800
192974	Neonatal alloimmune thrombocytopenia
192974	Glycoprotein Ia deficiency
224100	Congenital dyserythropoietic anemia II
230200	Galactokinase deficiency with cataracts
230800	Gaucher disease
230800	Gaucher disease with cardiovascular calcification

236730	Urofacial syndrome
249000	Meckel syndrome
253250	Mulibrey nanism
264470	Adrenoleukodystrophy, pseudoneonatal
266200	Anemia, hemolytic, due to PK deficiency
600140	Rubenstein-Taybi syndrome, 180849
600194	Ichthyosis bullosa of Siemens, 146800
600231	Palmoplantar keratoderma, Bothnia type
600273	Polycystic kidney disease, infantile severe, with tuberous sclerosis
600281	Non-insulin-dependent diabetes mellitus, 125853
600281	MODY, type 1, 125850
600584	Atrial septal defect with atrioventricular conduction defects, 108900
600808	Enuresis, nocturnal, 2
600897	Cataract, zonular pulverulent-1, 116200
600957	Persistent Mullerian duct syndrome, type I, 261550
601002	5-oxoprolinuria, 266130
601002	Hemolytic anemia due to glutathione synthetase deficiency, 231900
601105	Pycnodysostosis, 265800
601146	Brachydactyly, type C, 113100
601146	Acromesomelic dysplasia, Hunter-Thompson type, 201250
601146	Chondrodysplasia, Grebe type, 200700
601238	Cerebellar ataxia, Cayman type
601284	Hereditary hemorrhagic telangiectasia-2, 600376
601313	Polycystic kidney disease, adult type I, 173900
601412	Deafness, autosomal dominant 7
601493	Cardiomyopathy, dilated 1C
601596	Charcot-Marie-Tooth neuropathy, demyelinating
601652	Glaucoma 1A, primary open angle, juvenile-onset, 137750
601769	Osteoporosis, involutional
601769	Rickets, vitamin D-resistant, 277440
601785	Carbohydrate-deficient glycoprotein syndrome, type I, 212065
601846	Muscular dystrophy with rimmed vacuoles
602116	Glioma
602136	Refsum disease, infantile, 266510
602136	Zellweger syndrome-1, 214100
602136	Adrenoleukodystrophy, neonatal, 202370
602216	Peutz-Jeghers syndrome, 175200
602447	Coronary artery disease, susceptibility to
602477	Febrile convulsions, familial, 2
602491	Hyperlipidemia, familial combined, 1
602782	Faisalabad histiocytosis

Polynucleotide and Polypeptide Variants

[98] The present invention is directed to variants of the polynucleotide sequence disclosed in SEQ ID NO:X or the complementary strand thereto, nucleotide sequences encoding the polypeptide of SEQ ID NO:Y, the nucleotide sequence of SEQ ID NO:X encoding the polypeptide sequence as defined in column 7 of Table 1A, nucleotide sequences encoding the polypeptide as defined in column 7 of Table 1A, the nucleotide sequence as defined in columns 8 and 9 of Table 2, nucleotide sequences encoding the polypeptide encoded by the nucleotide sequence as defined in columns 8 and 9 of Table 2, the nucleotide sequence as defined in column 6 of Table 1B, nucleotide sequences encoding the polypeptide encoded by the nucleotide sequence as defined in column 6 of Table 1B, the cDNA sequence contained in Clone ID NO:Z, and/or nucleotide sequences encoding the polypeptide encoded by the cDNA sequence contained in Clone ID NO:Z.

[99] The present invention also encompasses variants of the polypeptide sequence disclosed in SEQ ID NO:Y, the polypeptide sequence as defined in column 7 of Table 1A, a polypeptide sequence encoded by the polynucleotide sequence in SEQ ID NO:X, a polypeptide sequence encoded by the nucleotide sequence as defined in columns 8 and 9 of Table 2, a polypeptide sequence encoded by the nucleotide sequence as defined in column 6 of Table 1B, a polypeptide sequence encoded by the complement of the polynucleotide sequence in SEQ ID NO:X, and/or a polypeptide sequence encoded by the cDNA sequence contained in Clone ID NO:Z.

[100] "Variant" refers to a polynucleotide or polypeptide differing from the polynucleotide or polypeptide of the present invention, but retaining essential properties thereof. Generally, variants are overall closely similar, and, in many regions, identical to the polynucleotide or polypeptide of the present invention.

[101] Thus, one aspect of the invention provides an isolated nucleic acid molecule comprising, or alternatively consisting of, a polynucleotide having a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence described in SEQ ID NO:X or contained in the cDNA sequence of Clone ID NO:Z; (b) a nucleotide sequence in SEQ ID NO:X or the cDNA in Clone ID NO:Z which encodes the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Z; (c) a nucleotide sequence in SEQ ID NO:X or the cDNA in Clone ID NO:Z which encodes a mature polypeptide; (d) a nucleotide sequence in SEQ ID NO:X or the cDNA sequence of Clone ID NO:Z, which encodes a biologically active fragment of a polypeptide; (e) a nucleotide sequence in SEQ ID NO:X or the cDNA sequence of Clone ID NO:Z, which

encodes an antigenic fragment of a polypeptide; (f) a nucleotide sequence encoding a polypeptide comprising the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Z; (g) a nucleotide sequence encoding a mature polypeptide of the amino acid sequence of SEQ ID NO:Y or the amino acid sequence encoded by the cDNA in Clone ID NO:Z; (h) a nucleotide sequence encoding a biologically active fragment of a polypeptide having the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Z; (i) a nucleotide sequence encoding an antigenic fragment of a polypeptide having the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Z; and (j) a nucleotide sequence complementary to any of the nucleotide sequences in (a), (b), (c), (d), (e), (f), (g), (h), or (i) above.

[102] The present invention is also directed to nucleic acid molecules which comprise, or alternatively consist of, a nucleotide sequence which is at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100%, identical to, for example, any of the nucleotide sequences in (a), (b), (c), (d), (e), (f), (g), (h), (i), or (j) above, the nucleotide coding sequence in SEQ ID NO:X or the complementary strand thereto, the nucleotide coding sequence of the cDNA contained in Clone ID NO:Z or the complementary strand thereto, a nucleotide sequence encoding the polypeptide of SEQ ID NO:Y, a nucleotide sequence encoding a polypeptide sequence encoded by the nucleotide sequence in SEQ ID NO:X, a polypeptide sequence encoded by the complement of the polynucleotide sequence in SEQ ID NO:X, a nucleotide sequence encoding the polypeptide encoded by the cDNA contained in Clone ID NO:Z, the nucleotide coding sequence in SEQ ID NO:X as defined in columns 8 and 9 of Table 2 or the complementary strand thereto, a nucleotide sequence encoding the polypeptide encoded by the nucleotide sequence in SEQ ID NO:X as defined in columns 8 and 9 of Table 2 or the complementary strand thereto, the nucleotide coding sequence in SEQ ID NO:B as defined in column 6 of Table 1B or the complementary strand thereto, a nucleotide sequence encoding the polypeptide encoded by the nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B or the complementary strand thereto, the nucleotide sequence in SEQ ID NO:X encoding the polypeptide sequence as defined in column 7 of Table 1A or the complementary strand thereto, nucleotide sequences encoding the polypeptide as defined in column 7 of Table 1A or the complementary strand thereto, and/or polynucleotide fragments of any of these nucleic acid molecules (e.g., those fragments described herein). Polynucleotides which hybridize to the complement of these nucleic acid molecules under stringent hybridization

conditions or alternatively, under lower stringency conditions, are also encompassed by the invention, as are polypeptides encoded by these polynucleotides and nucleic acids.

[103] In a preferred embodiment, the invention encompasses nucleic acid molecules which comprise, or alternatively, consist of a polynucleotide which hybridizes under stringent hybridization conditions, or alternatively, under lower stringency conditions, to a polynucleotide in (a), (b), (c), (d), (e), (f), (g), (h), or (i), above, as are polypeptides encoded by these polynucleotides. In another preferred embodiment, polynucleotides which hybridize to the complement of these nucleic acid molecules under stringent hybridization conditions, or alternatively, under lower stringency conditions, are also encompassed by the invention, as are polypeptides encoded by these polynucleotides.

[104] In another embodiment, the invention provides a purified protein comprising, or alternatively consisting of, a polypeptide having an amino acid sequence selected from the group consisting of: (a) the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Z; (b) the amino acid sequence of a mature form of a polypeptide having the amino acid sequence of SEQ ID NO:Y or the amino acid sequence encoded by the cDNA in Clone ID NO:Z; (c) the amino acid sequence of a biologically active fragment of a polypeptide having the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Z; and (d) the amino acid sequence of an antigenic fragment of a polypeptide having the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Z.

[105] The present invention is also directed to proteins which comprise, or alternatively consist of, an amino acid sequence which is at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100%, identical to, for example, any of the amino acid sequences in (a), (b), (c), or (d), above, the amino acid sequence shown in SEQ ID NO:Y, the amino acid sequence encoded by the cDNA contained in Clone ID NO:Z, the amino acid sequence of the polypeptide encoded by the nucleotide sequence in SEQ ID NO:X as defined in columns 8 and 9 of Table 2, the amino acid sequence of the polypeptide encoded by the nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B, the amino acid sequence as defined in column 7 of Table 1A, an amino acid sequence encoded by the nucleotide sequence in SEQ ID NO:X, and an amino acid sequence encoded by the complement of the polynucleotide sequence in SEQ ID NO:X. Fragments of these polypeptides are also provided (e.g., those fragments described herein). Further proteins encoded by

polynucleotides which hybridize to the complement of the nucleic acid molecules encoding these amino acid sequences under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention, as are the polynucleotides encoding these proteins.

[106] By a nucleic acid having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the nucleic acid is identical to the reference sequence except that the nucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the polypeptide. In other words, to obtain a nucleic acid having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. The query sequence may be an entire sequence referred to in Table 1A or 2 as the ORF (open reading frame), or any fragment specified as described herein.

[107] As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the present invention can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. 6:237-245 (1990)). In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be compared by converting U's to T's. The result of said global sequence alignment is expressed as percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identity are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, Window Size=500 or the length of the subject nucleotide sequence, whichever is shorter.

[108] If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for 5' and 3' truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5'

or 3' ends, relative to the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only bases outside the 5' and 3' bases of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

[109] For example, a 90 base subject sequence is aligned to a 100 base query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignment of the first 10 bases at 5' end. The 10 unpaired bases represent 10% of the sequence (number of bases at the 5' and 3' ends not matched/total number of bases in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 bases were perfectly matched the final percent identity would be 90%. In another example, a 90 base subject sequence is compared with a 100 base query sequence. This time the deletions are internal deletions so that there are no bases on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only bases 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to be made for the purposes of the present invention.

[110] By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that the subject polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query amino acid sequence, up to 5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the

reference sequence or in one or more contiguous groups within the reference sequence.

[111] As a practical matter, whether any particular polypeptide is at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequence of a polypeptide referred to in Table 1A (e.g., the amino acid sequence identified in column 6) or Table 2 (e.g., the amino acid sequence of the polypeptide encoded by the polynucleotide sequence defined in columns 8 and 9 of Table 2) or a fragment thereof, the amino acid sequence of the polypeptide encoded by the polynucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B or a fragment thereof, the amino acid sequence of the polypeptide encoded by the nucleotide sequence in SEQ ID NO:X or a fragment thereof, or the amino acid sequence of the polypeptide encoded by cDNA contained in Clone ID NO:Z, or a fragment thereof, can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci.6:237-245 (1990)). In a sequence alignment the query and subject sequences are either both nucleotide sequences or both amino acid sequences. The result of said global sequence alignment is expressed as percent identity. Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the subject amino acid sequence, whichever is shorter.

[112] If the subject sequence is shorter than the query sequence due to N- or C-terminal deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity. For subject sequences truncated at the N- and C-termini, relative to the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues

to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are considered for the purposes of manually adjusting the percent identity score. That is, only query residue positions outside the farthest N- and C- terminal residues of the subject sequence.

[113] For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-terminus of the subject sequence and therefore, the FASTDB alignment does not show a matching/alignment of the first 10 residues at the N-terminus. The 10 unpaired residues represent 10% of the sequence (number of residues at the N- and C- termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence. This time the deletions are internal deletions so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to be made for the purposes of the present invention.

[114] The polynucleotide variants of the invention may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce silent substitutions, additions, or deletions, but do not alter the properties or activities of the encoded polypeptide. Nucleotide variants produced by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, polypeptide variants in which less than 50, less than 40, less than 30, less than 20, less than 10, or 5-50, 5-25, 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also preferred. Polynucleotide variants can be produced for a variety of reasons, e.g., to optimize codon expression for a particular host (change codons in the human mRNA to those preferred by a bacterial host such as *E. coli*).

[115] Naturally occurring variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. (Genes II, Lewin, B., ed., John Wiley & Sons, New York (1985)). These allelic variants can vary at either the polynucleotide and/or polypeptide level and are included in the present invention.